

Db 6 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQPPGKGLWGIYVYSGSTNPNPSL 63  
QY 62 KSRVTMSVTSKRNHSLRLSSVTAADTAVYICAR--SDG-YTLDNWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARWGGDGFYAMDYWGQGLTVTVSS 119

## RESULT 5

US-09-025-769B-65  
; Sequence 65, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Prd. No. 2.3e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQPPGKGLWGIYVYSGSTNPNPSL 61  
Db 6 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQPPGKGLWGIYVYSGSTNPNPSL 63  
QY 62 KSRVTMSVTSKRNHSLRLSSVTAADTAVYICAR--SDG-YTLDNWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARWGGDGFYAMDYWGQGLTVTVSS 119

## RESULT 6

US-08-360-125-11  
; Sequence 11, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA

APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246hiiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE: Hybridoma producing human antibody 1-3-1  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:

VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11

Query Match 80.8%; Score 496; DB 1; Length 122;  
Best Local Similarity 81.2%; Pred. No. 1.le-42;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 2 ESGPLVKPSQTLSLCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYNPSL 61  
Db 6 ESGPLVKPSQTLSLCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD----GYTLDNWGQGLTVTVSS 114  
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARGSYGGYYGMDVWGQGLTVTVSS 122

RESULT 7  
US-08-450-578-11  
; Sequence 11, Application US/08450578  
; Patent No. 5837845  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5837845ihiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,578  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/360,125  
; FILING DATE: December 20, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-9850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11

Query Match 80.8%; Score 496; DB 2; Length 122;  
Best Local Similarity 81.2%; Pred. No. 1.le-42;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 2 ESGPLVKPSQTLSLCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYNPSL 61  
Db 6 ESGPLVKPSQTLSLCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD----GYTLDNWGQGLTVTVSS 114  
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARGSYGGYYGMDVWGQGLTVTVSS 122

RESULT 8  
US-09-017-628-11  
; Sequence 11, Application US/09017628  
; Patent No. 5990287  
; GENERAL INFORMATION:  
; APPLICANT: HOSOKAWA, Saiko  
; APPLICANT: TAGAWA, Toshiaki  
; APPLICANT: HIRAKAWA, Yoko  
; APPLICANT: ITO, No. 5990287ihiko  
; APPLICANT: NAGAIKE, Kazuhiro  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
; FILE REFERENCE: 177/527361KH  
; CURRENT APPLICATION NUMBER: US/09/017,628  
; CURRENT FILING DATE: 1998-02-02  
; EARLIER APPLICATION NUMBER: 08/360,125  
; EARLIER FILING DATE: 1994-12-20  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 11

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; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.le-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSTLSLTCTVSGSIRSGGYWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSTLSLTCTVSGSIRSGGYWIRQPPGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLSSVTAADTAVYYCARSD----GYTLDNWQGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGSGYGYGMDVMGQGTIVTVSS 122

RESULT 9
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.le-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSTLSLTCTVSGSIRSGGYWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSTLSLTCTVSGSIRSGGYWIRQPPGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLSSVTAADTAVYYCARSD----GYTLDNWQGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGSGYGYGMDVMGQGTIVTVSS 122

RESULT 10
US-08-450-363-11
; Sequence 11, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
```





GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 57672461hiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:

AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-5  
Query Match 79.4%; Score 487.5; DB 1; Length 119;  
Best Local Similarity 81.6%; Pred. No. 7.4e-42;  
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;  
Qy 2 ESGPLVKPSQTLSTCTVSGGSIRSGYYSWIRQPGKLEWIGYIYSGTYNPSL 61  
Db 6 ESGPLVKPSQTLSTCTVSGGSIRSGYYSWIRQPGKLEWIGYIYSGTYNPSL 65  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNWGQGTLTVSS 114  
Db 66 KSRVTISLDTSKQFSLKLSLTAADTAVYYCARSTRLRGADYWGQGTMTVSS 119  
RESULT 14  
US-08-450-578-5  
Sequence 5, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
US-08-450-578-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 7.4e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWWSWIRQPPGKGLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWWSWIRQPPGKGLEWIGYIYHSGNTYINPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNWGQGLTVTVSS 114
Db 66 KSRVTISLDTSKSQFSLKLSLTAADTAVYYCARSTRRLRGADYWGQGTMTVTSS 119

Search completed: August 8, 2004, 12:20:24
Job time : 13.6455 secs

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
US-09-017-628-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 7.4e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWWSWIRQPPGKGLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWWSWIRQPPGKGLEWIGYIYHSGNTYINPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNWGQGLTVTVSS 114
Db 66 KSRVTISLDTSKSQFSLKLSLTAADTAVYYCARSTRRLRGADYWGQGTMTVTSS 119

RESULT 15
US-09-017-628-5
; Sequence 5, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiko
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
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; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5
```

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Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 7.4e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWWSWIRQPPGKGLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWWSWIRQPPGKGLEWIGYIYHSGNTYINPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNWGQGLTVTVSS 114
Db 66 KSRVTISLDTSKSQFSLKLSLTAADTAVYYCARSTRRLRGADYWGQGTMTVTSS 119
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Search completed: August 8, 2004, 12:20:24  
Job time : 13.6455 secs



Best Local Similarity 85.7%; Pred. No. 1.1e-35;  
Matches 90; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 60

DB 19 QMTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 78

QY 61 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 105

DB 79 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 123

## RESULT 3

B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C:Accession: B49047

R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Eur. J. Immunol. 22, 2231-2236, 1992

A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes

A:Reference number: A49047; PMID:92387224; PMID:1516616

A:Accession: B49047

A:Molecule type: preliminary

A:Status: preliminary

A:Residues: 1-108 <VIC>

A:Experimental source: thymic B lymphocytes

A:Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 458; DB 2; Length 108;

Best Local Similarity 84.9%; Pred. No. 1.2e-35; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 60

DB 3 QMTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 106

DB 63 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 108

## RESULT 4

S47182

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S47182

R:McIntosh, R.S.; Randon, N.; Metcalfe, R.A.; Weetman, A.P.

submitted to the EMBL Data Library, June 1994

A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient

A:Reference number: S47181

A:Accession: S47182

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <MC1>

A:Cross-references: EMBL:X79786; NID:G506422; PIDN:CAA56182.1; PID:G506423

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;

Best Local Similarity 84.9%; Pred. No. 1.8e-35; Indels 0; Gaps 0;

Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 60

DB 3 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 106

DB 63 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 108

DB 63 SGSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 108

## RESULT 5

S31979

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S31979

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL Data Library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations

A:Reference number: S31977

A:Accession: S31979

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: EMBL:Z15075; NID:G38489; PIDN:CAA78784.1; PID:G38490

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;

Best Local Similarity 81.9%; Pred. No. 4.4e-35;

Matches 86; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 61

DB 4 MTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 63

QY 62 GSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 106

DB 64 GSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 108

## RESULT 6

S31998

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S31998

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL Data Library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations

A:Reference number: S31977

A:Accession: S31998

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;

Best Local Similarity 83.8%; Pred. No. 4.4e-35;

Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 61

DB 4 MTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKGKAPKLLIYAASSLSQGVPSRF 63

QY 62 GSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 106

DB 64 GSGYGTDTLTITSSSQFEDFASYCQESLSASYTFQGTQKVEIK 108

## RESULT 7

S31980

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S31980; S32000





GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 5.78192 Seconds  
(without alignments)  
954.620 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGRVTIS.....QESLSASYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	436	80.3	129	1	P04431 homo sapien
2	433	79.7	108	1	KV1E_HUMAN
3	430	79.2	108	1	KV1H_HUMAN
4	420	77.3	108	1	KV1N_HUMAN
5	416	76.6	108	1	KV1P_HUMAN
6	414	76.2	108	1	KV1K_HUMAN
7	413	76.1	108	1	KV1V_HUMAN
8	412	75.9	108	1	KV1O_HUMAN
9	409	75.3	108	1	KV1G_HUMAN
10	408	75.1	108	1	KV1B_HUMAN
11	407	75.0	108	1	KV1M_HUMAN
12	406	74.8	108	1	KV1R_HUMAN
13	404	74.4	108	1	KV1A_HUMAN
14	399.5	73.6	107	1	KV1D_HUMAN
15	399	73.5	108	1	KV1S_HUMAN
16	398	73.3	108	1	KV1P_HUMAN
17	397	73.1	108	1	KV1L_HUMAN
18	397	73.1	129	1	KV1X_HUMAN
19	396	72.9	108	1	KV1Y_HUMAN
20	391	72.0	108	1	KV1Q_HUMAN
21	385.5	71.0	109	1	KV1T_HUMAN
22	384	70.7	108	1	KV1C_HUMAN
23	376	69.2	108	1	KV5T_MOUSE
24	373	68.7	108	1	KV5S_MOUSE
25	370.5	68.2	109	1	KV3E_HUMAN
26	370	68.1	108	1	KV5Q_MOUSE
27	368.5	67.9	109	1	KV3B_HUMAN
28	368.5	67.9	109	1	KV3D_HUMAN
29	368	67.8	108	1	KV5N_MOUSE
30	368	67.8	108	1	KV5O_MOUSE
31	368	67.8	117	1	KV1J_HUMAN
32	367.5	67.7	129	1	KV3M_HUMAN
33	366.5	67.5	129	1	KV3L_HUMAN

34	366	67.4	114	1	KV4A_HUMAN	P01625 homo sapien
35	366	67.4	117	1	KV1I_HUMAN	P01601 homo sapien
36	365	67.2	108	1	KV5K_MOUSE	P01644 mus musculus
37	365	67.2	108	1	KV5M_MOUSE	P01646 mus musculus
38	365	67.2	134	1	KV4C_HUMAN	P06314 homo sapien
39	364	67.0	108	1	KV5R_MOUSE	P01651 mus musculus
40	363	66.9	111	1	KV3M_MOUSE	P01665 mus musculus
41	362	66.7	111	1	KV3L_MOUSE	P01664 mus musculus
42	361	66.5	108	1	KV5P_MOUSE	P01649 mus musculus
43	360	66.3	108	1	KV5L_MOUSE	P01645 mus musculus
44	358	65.9	111	1	KV3O_MOUSE	P01667 mus musculus
45	357	65.7	128	1	KV5E_MOUSE	P01637 mus musculus

## ALIGNMENTS

### RESULT 1

KV1W\_HUMAN  
ID KV1W\_HUMAN STANDARD; PRT; 129 AA.  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014146; PubMed=6091049;  
RA Klobeck H.G., Combratio G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related";  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X00965; CAA25477.1; ALT\_TERM.  
DR PIR; A01883; K1HUKW.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 129 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 80.3%; Score 436; DB 1; Length 129;  
Best Local Similarity 81.9%; Pred. No. 8.2e-40;  
Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQSGVPSRF 60  
 DB 25 QMTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQSGVTSRF 84

QY 61 SSGSGVGTDFTLTISLQFEDFASYCQESLSASYTFGQGTKEIKR 105  
 DB 85 SSGSGGTDFTLTISLQFEDFASYCQESLSASYTFGQGTKEIKR 129

## RESULT 2

KVLE HUMAN STANDARD; PRT; 108 AA.  
 ID KVLE HUMAN STANDARD; PRT; 108 AA.  
 AC P01597;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region DBE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72053133; PubMed=5124396;  
 RA Milstein C.P.; Deverson E.V.;  
 RT "The amino acid sequence of a human kappa light chain."  
 RL Biochem. J. 123:945-958(1971).  
 CC -/- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01865; KIHUDE.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 FRAMEWORK-4.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;  
 Best Local Similarity 77.4%; Pred. No. 1.4e-39;  
 Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQSGVPSRF 60  
 DB 3 ZMTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQSGVPSRF 62

QY 61 SSGSGVGTDFTLTISLQFEDFASYCQESLSASYTFGQGTKEIKR 106  
 DB 63 SSGSGGTDFTLTISLQFEDFASYCQESLSASYTFGQGTKEIKR 108

## RESULT 3

KVLI HUMAN STANDARD; PRT; 108 AA.  
 ID KVLI HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S.; Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
 subgroups."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
 CC -/- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01868; KIHURU.  
 DR HSSP; P80362; 1WTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 08D3A6160D8D0618 CRC64;

Query Match 79.2%; Score 430; DB 1; Length 108;  
 Best Local Similarity 78.3%; Pred. No. 3e-39;  
 Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQSGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQSGVPSRF 62  
 QY 61 SSGSGVGTDFTLTISLQFEDFASYCQESLSASYTFGQGTKEIKR 106  
 DB 63 SSGSGGTDFTLTISLQFEDFASYCQESLSASYTFGQGTKEIKR 108

## RESULT 4

KVIN HUMAN STANDARD; PRT; 108 AA.  
 ID KVIN HUMAN STANDARD; PRT; 108 AA.  
 AC P01606;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region OU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H.; Shimizu A.; Paul C.; Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 chains."  
 RL Science 169:56-59(1970).  
 CC -/- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -/- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM S  
 MACROGLOBULIN.  
 DR PIR; A01872; KIHUOU.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.



```

DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 99 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105927E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 3.5e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSTLSASVGDRTVITICRASZTISLYLWYZZKPGKAPBLLIYAASLHSGVPSRF 62

QY 61 SGSGVGTDFTLTISLQPEDFASYVCQBSLSASVYTFGGQTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTBTFTTISLZPZBFATYCYZSYSPPTFGZGTRIZIKR 108

RESULT 5
KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
EN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; KIHUEU.
DR HSSP; P01607; 1REI.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105927E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 3.5e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSTLSASVGDRTVITICRASZTISLYLWYZZKPGKAPBLLIYAASLHSGVPSRF 62

QY 61 SGSGVGTDFTLTISLQPEDFASYVCQBSLSASVYTFGGQTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTBTFTTISLZPZBFATYCYZSYSPPTFGZGTRIZIKR 108

RESULT 5
KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
EN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; KIHUEU.
DR HSSP; P01607; 1REI.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105927E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 3.5e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSTLSASVGDRTVITICRASZTISLYLWYZZKPGKAPBLLIYAASLHSGVPSRF 62

QY 61 SGSGVGTDFTLTISLQPEDFASYVCQBSLSASVYTFGGQTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTBTFTTISLZPZBFATYCYZSYSPPTFGZGTRIZIKR 108

RESULT 6
KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
EN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; 1WTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 76.2%; Score 414; DB 1; Length 108;
Best Local Similarity 70.8%; Pred. No. 1.5e-37;
Matches 75; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSTLSVSGDRVTITICRSTVLSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62

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FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11798 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.6%; Score 416; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 9.3e-38;
Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSTLSASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 62

QY 61 SGSGVGTDFTLTISLQPEDFASYVCQBSLSASVYTFGGQTKVEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 IGSQSGTEFTLTISLQPDFTATYCYQYNSDSKMFQGGTKVEIKR 107

RESULT 6
KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
EN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; 1WTL.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 76.2%; Score 414; DB 1; Length 108;
Best Local Similarity 70.8%; Pred. No. 1.5e-37;
Matches 75; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRASQRTINLYNQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSTLSVSGDRVTITICRSTVLSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62

```

OY 61 SSGSGYGTDFLTLSLQFDFASYYCOESLSASVTFGGQTKVIEKR 106  
 DB 63 SQGSGTBTFTTSSVZPZFAFYCYQZYLDLPRFGQTKVDLKR 108

## RESULT 7

KV10 HUMAN STANDARD; PRT; 108 AA.  
 AC P04430;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region BAN.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RZ SEQUENCE.  
 RP MEDLINE=86174817; PubMed=3083240;  
 RA Dwalet F.E., O'Connor T.P., Benson M.D.;  
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
 RL Mol. Immunol. 23:73-78(1986).  
 DR PIR; A01878; KIHUBN.  
 DR HSP; P80362; IWLTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR PIR; P80047; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region; Amyloid.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DOMAIN 108 108  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 76.1%; Score 413; DB 1; Length 108;  
 Best Local Similarity 76.4%; Pred. No. 2e-37;  
 Matches 81; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGDRTVITSCRASQRTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60  
 DB 3 QLTQSPSSLSASVGDRTVITSCRASQSVYVAVFQKPGKAPKSLIYDASTLQSGVPSNF 62

OY 61 SSGSGYGTDFLTLSLQFDFASYYCOESLSASVTFGGQTKVIEKR 106  
 DB 63 TSGSGGTDFLTLSLQFDFASYYCOQVNSYPTFGQTKVQIKR 108

## RESULT 8

KV10 HUMAN STANDARD; PRT; 108 AA.  
 ID P01607;  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE Ig kappa chain V-I region Rel.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RZ SEQUENCE.  
 RP MEDLINE=76023758; PubMed=809329;

RA "The primary structure of a crystalline monoclonal immunoglobulin  
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Re1); isolation  
 RT and characterization of the tryptic peptides; the complete amino acid  
 RT sequence of the protein; a contribution to the elucidation of the  
 RT three-dimensional structure of antibodies, in particular their  
 RT combining site.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039968; PubMed=1182131;  
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 RT of the Bence-Jones protein RE1 refined at 2.0-A resolution.";  
 RL Biochemistry 14:4943-4952(1975).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR; A91663; KIHURE.  
 DR PDB; 1REI; 17-FEB-84.  
 DR PDB; 1AR2; 12-NOV-97.  
 DR PDB; 1BWW; 29-DEC-99.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR PIR; P80047; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 44 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 85 90  
 FT STRAND 97 98  
 FT STRAND 102 106  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 75.9%; Score 412; DB 1; Length 108;  
 Best Local Similarity 75.5%; Pred. No. 2.5e-37;  
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGDRTVITSCRASQRTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60  
 DB 3 QLTQSPSSLSASVGDRTVITSCRASQDIKLYLNWYQTPGKAPKLLIYASNLOQVPSRF 62

OY 61 SSGSGYGTDFLTLSLQFDFASYYCOESLSASVTFGGQTKVIEKR 106  
 DB 63 SSGSGGTDFLTLSLQFDFATYYCOYQSLPYTFGGTKLQITR 108

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RESULT 9
KV1G_HUMAN
ID_KV1G_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
  (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
  kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
  MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CF600FF73 CRC64;

Query Match 75.3%; Score 409; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 5.3e-37;
Matches 83; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVITISCRASQRTINTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVITISCRASQRTINTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 62

Qy 61 SGSGYGTDFLTITISLQPEDFASVYQESLSASVTFGGQTKVEIKR 106
Db 63 SGSGAGTEFTITISLQPEDFATYICLQNSYPRSFQGTKEIKR 108

RESULT 10
KV1M_HUMAN
ID_KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
  immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
  protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
  Bence-Jones protein Au.";
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EX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
  IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
  specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
  CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
  WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
  GLOBULIN ACTIVITY.
DR PIR; A01871; KIHULY.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 75.1%; Score 408; DB 1; Length 108;
Best Local Similarity 73.6%; Pred. No. 6.7e-37;
Matches 78; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVITISCRASQRTINTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVITISCRASQRTINTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 62

Qy 61 SGSGYGTDFLTITISLQPEDFASVYQESLSASVTFGGQTKVEIKR 106
Db 63 SGSGGTDFTITISLQPEDIAIYICQYNNWPFPGQTKVEIKR 108

RESULT 11
KV1B_HUMAN
ID_KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
  immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
  protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
  Bence-Jones protein Au.";
```

RL Biophys. Struct. Mech. 1:139-146 (1975).  
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A91653; KIHUAG.  
DR PDB; 1UV5; 30-JAN-02.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 89 97 FRAMEWORK-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DOMAIN 108 108 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6F6B99 CRC64;  
Query Match 75.0%; Score 407; DB 1; Length 108;  
Best Local Similarity 75.5%; Pred. No. 8.6e-37;  
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGRVITICRASQIRNLTWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
DB 3 QMTQSPSSLSASVGRVITICRASQIRNLTWYQKPGKAPKLLIYAASSLSQSGVPSRF 62  
QY 61 SSGSGYGTFTLTISLQPEDFASYCQESLSASYTFGQGTKEIKR 106  
DB 63 SSGSGYGTFTLTISLQPEDFATYCCQYDYLPTWFGQGTKEIKR 108  
RESULT 12  
KVLR HUMAN STANDARD; PRT; 108 AA.  
AC P01610;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region WEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Goni F.; Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
RT (protein WEA) with antibody activity against 3,4-pyruvylated  
RT galactose in Klebsiella polysaccharides K30 and K33.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
CC WALDENSTROM'S MACROGLOBULINEMIA.  
DR PIR; A01876; KIHUAG.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Monoclonal antibody.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DOMAIN 108 108 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;  
Query Match 74.8%; Score 406; DB 1; Length 108;  
Best Local Similarity 75.5%; Pred. No. 1.1e-36;  
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGRVITICRASQIRNLTWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
DB 3 QMTQSPSSLSASVGRVITICRASQIRNLTWYQKPGKAPKLLIYAASSLSQSGVPSRF 62  
QY 61 SSGSGYGTFTLTISLQPEDFASYCQESLSASYTFGQGTKEIKR 106  
DB 63 SSGSGYGTFTLTISLQPEDFATYCCQYDYLPTWFGQGTKEIKR 108  
RESULT 13  
KVLA HUMAN STANDARD; PRT; 108 AA.  
AC P01593;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region AG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=69234734; PubMed=4893682;  
RA Titani K.; Shinoda T.; Putnam F.W.;  
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
RT complete sequence and the location of the disulfide bridges.";  
RL J. Biol. Chem. 244:3550-3560 (1969).  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR PIR; A01861; KIHUAG.  
DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DOMAIN 108 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;  
Query Match 74.4%; Score 404; DB 1; Length 108;  
Best Local Similarity 73.6%; Pred. No. 1.8e-36;  
Matches 78; Conservative 13; Mismatches 15; Indels 0; Gaps 0;





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 29.0697 Seconds  
(without alignments)  
1150.508 Million cell updates/sec

Title: US-10-027-725A-10  
Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGDVRTIS.....QESLSASTFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	465	85.6	108	Q9UL77	Q9UL77 homo sapien
2	449.5	82.8	107	Q96SA9	Q96SA9 homo sapien
3	439.5	80.9	107	Q9UL81	Q9UL81 homo sapien
4	422	77.7	108	Q9UL79	Q9UL79 homo sapien
5	420	77.3	108	Q9UL70	Q9UL70 homo sapien
6	418	77.0	234	Q7Z473	Q7Z473 homo sapien
7	412	75.9	236	Q7Z3Y4	Q7Z3Y4 homo sapien
8	371	68.3	108	Q9UL83	Q9UL83 homo sapien
9	371	68.3	116	Q96PF6	Q96PF6 homo sapien
10	366	67.4	298	Q9QVF0	Q9QVF0 mus musculus
11	364	67.0	214	Q9RIA5	Q9RIA5 mus musculus
12	361	66.5	234	Q91WF8	Q91WF8 mus musculus
13	361	66.5	234	Q8R062	Q8R062 mus musculus
14	361	66.5	236	Q7TMK3	Q7TMK3 mus musculus
15	359	66.1	109	Q920E6	Q920E6 mus musculus
16	359	66.1	111	Q920E9	Q920E9 mus musculus

17	357	65.7	233	11	Q91WS9	Q91ws9 mus musculus
18	357	65.7	234	11	Q8VCP0	Q8vcp0 mus musculus
19	355.5	109	4	Q9UL78	Q9ul78 homo sapien	
20	354	65.2	236	11	Q7TS98	Q7ts98 mus musculus
21	350	64.5	111	11	Q811U6	Q811u6 mus musculus
22	346.5	63.8	109	4	Q9UL86	Q9ul86 homo sapien
23	346	63.7	108	11	Q8V1D0	Q8v1d0 mus musculus
24	345.5	63.6	109	4	Q9UL85	Q9ul85 homo sapien
25	335.5	61.8	243	11	Q7TQM2	Q7tqm2 mus musculus
26	332.5	61.2	112	11	Q8K1F3	Q8k1f3 mus musculus
27	332.5	61.2	235	11	Q7TMK0	Q7tmk0 mus musculus
28	332	61.1	107	11	Q9ER29	Q9er29 mus musculus
29	330.5	60.9	238	11	Q99M37	Q99m37 mus musculus
30	329.5	60.7	114	11	Q8K1F1	Q8k1f1 mus musculus
31	328	60.4	127	11	Q925S9	Q925s9 mus musculus
32	328	60.4	131	11	Q811C3	Q811c3 mus musculus
33	325.5	59.9	112	11	Q8K1F2	Q8k1f2 mus musculus
34	323	59.5	99	11	Q9JL74	Q9jl74 mus musculus
35	321.5	59.2	238	11	Q8VC16	Q8vc16 mus musculus
36	320.5	59.0	134	11	Q8VDD0	Q8vdd0 mus musculus
37	320.5	59.0	241	11	Q921A6	Q921a6 mus musculus
38	319	58.7	107	11	Q9JL84	Q9jl84 mus musculus
39	317	58.4	237	13	Q7SZ36	Q7sz36 xenopus lae
40	315	58.0	103	11	Q9JL80	Q9jl80 mus musculus
41	314.5	57.9	239	4	Q8NEK0	Q8nek0 homo sapien
42	311.5	57.4	106	5	Q9U410	Q9u410 schistosoma
43	308	56.7	234	11	Q8R028	Q8r028 mus musculus
44	307.5	56.6	239	11	Q8VC55	Q8vc55 mus musculus
45	305.5	56.3	104	11	Q9JL82	Q9jl82 mus musculus

## ALIGNMENTS

RESULT 1

Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1; -.  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF000047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 85.6%; Score 465; DB 4; Length 108;  
Best Local Similarity 84.9%; Pred. No. 1.7e-44;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVRTISCRASQRIINTYVQHPGKAPKLLIYAASSLOSQGVPSRF 60

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Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGYGTDTLTITSSLOPEDFASYVCOESLSASVYTFQGTGKVEIKR 106
Db 63 SSGSGGTDTLTITSSLOPEDFATYVCOESYSYTSWTFEGTKVEIKR 108

RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9875893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 82.8%; Score 449.5; DB 4; Length 107;
Best Local Similarity 84.9%; Pred. No. 9.1e-43;
Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGTDTLTITSSLOPEDFASYVCOESLSASVYTFQGTGKVEIKR 106
Db 63 SSGSGGTDTLTITSSLOPEDFATYVCOESYSYTSWTFEGTKVEIKR 107

RESULT 3
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic
RT arthritis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 77.7%; Score 422; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 61
Db 4 MTQSPSLLSASTGDRVTISCRMSQGISYLAWYQKPKAPKAPKLLIYAASSLSQGVPSRF 63

QY 62 GSGYGTDTLTITSSLOPEDFASYVCOESLSASVYTFQGTGKVEIKR 106
Db 64 GSGSGTDTLTITSSLOPEDFATYVCOESYSYTSWTFEGTKVEIKR 108

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RT "Myosin-reactive autoantibodies in rheumatic arthritis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 80.9%; Score 439.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.2e-41;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGTDTLTITSSLOPEDFASYVCOESLSASVYTFQGTGKVEIKR 106
Db 63 SSGSGTDTLTITSSLOPEDFATYVCOESYSYTSWTFEGTKVEIKR 107

RESULT 4
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic arthritis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 77.7%; Score 422; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPKAPKAPKLLIYAASSLSQGVPSRF 61
Db 4 MTQSPSLLSASTGDRVTISCRMSQGISYLAWYQKPKAPKAPKLLIYAASSLSQGVPSRF 63

QY 62 GSGYGTDTLTITSSLOPEDFASYVCOESLSASVYTFQGTGKVEIKR 106
Db 64 GSGSGTDTLTITSSLOPEDFATYVCOESYSYTSWTFEGTKVEIKR 108

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RESULT 5
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAS6280.1; -.
DR FJ; PH0863; PH0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 77.3%; Score 420; DB 4; Length 108;
Best Local Similarity 79.2%; Pred. No. 1.9e-39;
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVRVTISCRASORINTYLNWYQKPGKAPKLIYAASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGDVRVTITCRASGISYLAWYQKPGKAPKLIYAASSLSQGVPSRF 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GSGYGTDTLTITSLQFEDFASYVCQESLSASYTFGGQTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GSGSGTDTLTITSLQFEDVATYVCQKYNAPRTFGPGTKLEIKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWenley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWenley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC005332; AAH05332.1; -.

```

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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFAED23084BC6 CRC64;

Query Match
Best Local Similarity 75.9%; Score 412; DB 4; Length 236;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVISCASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITCRASQDIGNYLAWFQOKPGKAPKLLIYGASSLSQSGVQSKF 84
QY 61 GSGSGTDFTLTISSLPQEDFASYCQBSLSASVYFGQGTKEIKR 106
DB 85 GSGSGTDFTLTISSLPQEDFATYCCQYKSPVTFGGTKLEIKR 130

RESULT 8
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.B., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL: AF035031; AD56267.1; -.
DR PIR: B30609; S30609.
DR PIR: C30609; C30609.
DR PIR: D30609; D30609.
DR PIR: S34098; S34098.
DR PIR: S34099; S34099.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9FC5A92EBA96BEA CRC64;

Query Match
Best Local Similarity 68.3%; Score 371; DB 4; Length 108;
Matches 69; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
DB 4 MTQSPATLSVSPGERATLSCRASQSVSNLAWFQOKPGQAPRLLIYCASTRATGIPARFS 63
QY 62 GSGSGTDFTLTISSLPQEDFASYCQBSLSASVYFGQGTKEIKR 106
DB 64 GSGSGTDFTLTISSLPQEDFATYCCQYKSPVTFGGTKLEIKR 130

RESULT 9
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFAED23084BC6 CRC64;

Query Match
Best Local Similarity 75.9%; Score 412; DB 4; Length 236;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVISCASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITCRASQDIGNYLAWFQOKPGKAPKLLIYGASSLSQSGVQSKF 84
QY 61 GSGSGTDFTLTISSLPQEDFASYCQBSLSASVYFGQGTKEIKR 106
DB 85 GSGSGTDFTLTISSLPQEDFATYCCQYKSPVTFGGTKLEIKR 130

RESULT 8
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.B., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL: AF035031; AD56267.1; -.
DR PIR: B30609; S30609.
DR PIR: C30609; C30609.
DR PIR: D30609; D30609.
DR PIR: S34098; S34098.
DR PIR: S34099; S34099.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9FC5A92EBA96BEA CRC64;

Query Match
Best Local Similarity 68.3%; Score 371; DB 4; Length 108;
Matches 69; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
DB 4 MTQSPATLSVSPGERATLSCRASQSVSNLAWFQOKPGQAPRLLIYCASTRATGIPARFS 63
QY 62 GSGSGTDFTLTISSLPQEDFASYCQBSLSASVYFGQGTKEIKR 106
DB 64 GSGSGTDFTLTISSLPQEDFATYCCQYKSPVTFGGTKLEIKR 130

RESULT 9
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

```
Kappa 1 light chain variable region (Fragment).
SDNKL
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RA "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden."
RL Blood 98:714-720(2001).
DR EMBL: AF361758; AAK51465.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match
Best Local Similarity 68.3%; Score 371; DB 4; Length 116;
Matches 72; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVISCASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITCRASQDIGNYLAWFQOKPGKAPKLLIYGASSLSQSGVQSKF 84
QY 61 GSGSGTDFTLTISSLPQEDFASYCQBSLSASVYFGQGTKEIKR 106
DB 63 GSGSGTDFTLTISSLPQEDFATYCCQYKSPVTFGGTKLEIKR 108

RESULT 10
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CN 8 scFv.
DE CN 8.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinozawa N., Demura T., Fukuda H.;
RA "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL: AS036341; BAA88633.1; -.
DR PIR: A33933; A33933.
DR PIR: S19112; S19112.
DR HSSP: P01607; 1REI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match
Best Local Similarity 67.4%; Score 366; DB 11; Length 298;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 ELTQSPSSLSASVGVETVITICRAGNIHNYLAWIQQKGKSPQLLVYNAKTLADGVPSRF 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCOESLSASYTFGGQTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 235 SSGSGGQYSLKINSLOPEDFGSYCYQHFWTTPYTFGGGTKLEIKR 280
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
Q91WF8 Q91AF5 PRELIMINARY; PRT; 214 AA.
AC Q91AF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RA "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -
DR PDB; 1C1C; 11-MAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K60; 16-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214 1
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 67.0%; Score 364; DB 11; Length 214;
Best Local Similarity 64.2%; Pred. No. 9.le-33;
Matches 68; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QLTQSPSSMYASLGERVITICKASQDINSYLSWFQQRFGKSPKLLIYRANLVDGVPSRF 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCOESLSASYTFGGQTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGQYSLTISSEYEDMGVIYCLQYDEFFPTFGSGTKLEIKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
Q91WF8 Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 2.2e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYTSLSHSGVPSRF 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCOESLSASYTFGGQTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTHYSLTISNLEPEDIATYCCQYSQFFPTFGSGTKLEIKR 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAHL5292.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; E0D0B0E6EB7812D2 CRC64;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 65.1%; Pred. No. 2.2e-32;
Matches 69; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYTSLSHSGVPSRF 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCOESLSASYTFGGQTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTHYSLTISNLEPEDIATYCCQGNTPPTFGSGTKLEIKR 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
Q9R062 Q9R062 PRELIMINARY; PRT; 234 AA.
AC Q9R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 2.2e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYTSLSHSGVPSRF 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYDFTLTITSSLOFEDFASYCOESLSASYTFGGQTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTHYSLTISNLEPEDIATYCCQYSQFFPTFGSGTKLEIKR 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14

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Search completed: August 8, 2004, 12:17:46  
Job time : 30.0697 secs

Search completed: August 8, 2004, 12:17:46  
Job time : 30.0697 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 43 5242 Seconds  
(without alignments)  
688.123 Million cell updates/sec

Title: US-10-027-725A-10  
Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFQGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	533	98.2	106	5	ABG30448 Human IGE
2	475	87.5	107	2	AAR54260 Anti-HIV
3	475	87.5	107	2	AAW01283 VL region
4	475	87.5	107	3	AAy98244 Anti-gp12
5	475	87.5	107	3	AAy95135 Anti-gp12
6	474	87.3	107	4	AAG93667 Human ant
7	474	87.3	107	6	ABO27474 Anti-Rh(D
8	472	86.9	107	4	AAG93663 Human ant
9	472	86.9	107	4	AAG93664 Human ant
10	472	86.9	107	4	AAG93590 Human ant
11	472	86.9	107	6	ABO27471 Anti-Rh(D
12	472	86.9	107	6	ABO27397 Anti-Rh(D
13	472	86.9	107	6	ABO27470 Anti-Rh(D
14	471	86.7	107	4	AAG93644 Human ant
15	471	86.7	107	6	ABO27451 Anti-Rh(D
16	468	86.2	107	4	AAG93593 Human ant
17	468	86.2	107	6	ABO27400 Anti-Rh(D
18	467	86.0	107	2	AAR54261 Anti-HIV
19	467	86.0	107	2	AAW01284 VL region
20	467	86.0	107	3	AAy98245 Anti-gp12
21	467	86.0	107	3	AAy95136 Anti-gp12
22	467	86.0	114	2	AAW13922 Light cha
23	465	85.6	111	4	AAG83656 Amino aci
24	465	85.6	111	6	ABJ38615 Hepatitis
25	465	85.6	132	2	AAW22842 Human ant

26	465	85.6	240	6	ABJ38595	Abj38595 Hepatitis
27	465	85.6	299	4	AAG63660	Amino aci
28	464.5	85.5	108	4	AAG93589	Human ant
29	464.5	85.5	108	4	AAG93600	Human ant
30	464.5	85.5	108	6	ABO27407	Anti-Rh(D
31	464.5	85.5	108	6	ABO27396	Anti-Rh(D
32	464	85.5	107	4	AAG93594	Human ant
33	464	85.5	107	6	ABO27401	Anti-Rh(D
34	464	85.5	108	6	ABP96009	HSA antib
35	464	85.5	240	2	AAy02472	A single
36	464	85.5	240	4	AAAB46007	Human MUC
37	464	85.5	240	4	AAAB46038	Human TP
38	464	85.5	240	4	AAAB46008	Human MUC
39	464	85.5	240	4	AAAB46006	Human MUC
40	464	85.5	240	4	AAAB46005	Human MUC
41	464	85.5	240	6	ABP95997	Human Ser
42	462	85.1	107	4	AAG93596	Human ant
43	462	85.1	107	4	AAG93595	Human ant
44	462	85.1	107	6	ABO27403	Anti-Rh(D
45	462	85.1	107	6	ABO27402	Anti-Rh(D

## ALIGNMENTS

RESULT 1  
ABG30448  
ID ABG30448 standard; protein; 106 AA.  
XX AC ABG30448;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human IGE Fab clone 94 light chain protein.  
XX  
KW Human; fab; anti-allergic; vaccine; grass pollen; phi p 2;  
KW timothy grass pollen allergen; passive immunotherapy.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..21 /note= "FR1 region"  
FT Region 22..32 /note= "CDR1 region"  
FT Region 33..47 /note= "FR2 region"  
FT Region 48..54 /note= "CDR2 protein"  
FT Region 55..86 /note= "FR3 region"  
FT Region 87..95 /note= "CDR2 region"  
FT Region 96..104 /note= "FR4 region"  
WO200253595-A1.  
11-JUL-2002.  
27-DEC-2001; 2001WO-SE002908.  
29-DEC-2000; 2000SE-00004892.  
(PHAA ) PHARMACIA DIAGNOSTICS AB.  
Flicker S, Steinberger P, Kraft D, Valenta R;  
WPI; 2002-583604/62.  
N-PSDB; ABK89640.  
Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental  
XX allergen detection.

PS Disclosure; Page 39; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
XX fab, clone 94 light chain protein of the invention

SQ Sequence 106 AA;

Query Match 98.2%; Score 533; DB 5; Length 106;  
Best Local Similarity 99.1%; Pred. No. 3.5e-33; Indels 0; Gaps 0;  
Matches 105; Conservative 0; Mismatches 1;

QY 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SGSGYGTDTLTITISSLOPDEFASYCQESLSASVTFGQGTKEIKR 106

DB 61 SGSGYGTDTLTITISSLOPDEFASYCQESLSASVTFGQGTKEIKR 106

RESULT 2

AAR54260

ID AAR54260 standard; protein; 107 AA.

XX AAR54260;

XX 25-MAR-2003 (revised)

DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b22.

DE Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
XX neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..21 /label= FR1

FT Region 22..33 /label= CDR1

FT Region 34..48 /label= FR2

FT Region 49..55 /label= FR2

FT Region 56..87 /label= CDR2

FT Region 88..95 /label= FR3

FT Region 96..107 /label= CDR3

FT Region 96..107 /label= FR4

XX WO9407922-A1.

XX 14-APR-1994.

XX

PF 30-SEP-1993; 93WO-US009328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or  
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro  
XX diagnosis and for passive immuno-therapy.

XX Claim 5; Page 189; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification  
CC using primers specific for heavy and light chain variable regions. The  
CC amplification products were inserted into a dicistronic vector to produce  
CC a library of fragments. E.coli XLI Blue cells were transformed with the  
CC library. Filamentous phage were produced which expressed the MAB regions  
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
CC immunoreactive clones. The light chain VK region sequence AAR54260  
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 107 AA;

Query Match 87.5%; Score 475; DB 2; Length 107;

Best Local Similarity 87.7%; Pred. No. 8.5e-29;

Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVSGDRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60

DB 1 ELTQSPSSLASVSGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SGSGYGTDTLTITISSLOPDEFASYCQESLSASVTFGQGTKEIKR 106

DB 61 SGSGYGTDTLTITISSLOPDEFATYCCQSYSTPTFTGQGTKEIKR 106

RESULT 3

AAW01283

ID AAW01283 standard; protein; 107 AA.

XX AAW01283;

XX 29-JAN-1997 (first entry)

XX VL region of HIV neutralising MAB, clone b22 and B35.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB;  
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;

XX anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..21 /label= FR1

FT Region 22..32 /label= CDR1

FT Region 33..47 /label= FR2

FT Region 48..54 /label= CDR2

FT Region 55..86 /label= FR3

FT Region 87..95 /label= CDR3

FT Region 96..107 /label= FR4

XX

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PN WO9602273-A1.
XX
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
XX immuno:therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366pp; English.
XX
XX The sequences given in AAW01261-92 represent the light chain variable
XX regions (VL) of a series of monoclonal antibodies (Mab's) which are
XX immunoreactive with HIV glycoprotein gp120 and are capable of
XX neutralising HIV. This sequence represents the sequence of the JK2 gene
XX clones, B22 and B35. A Mab containing this VL sequence has the capacity
XX to reduce HIV infectivity titre in an in vivo virus infectivity assay by
XX 50 % at a concentration of less than 700 ng of antibody/ml, and binds
XX mature gp120 preferentially over the precursor gp160. The Mab may be used
XX for determining immunocompetence of a human anti-HIV antibody and in the
XX detection of HIV infection
XX
XX Sequence 107 AA;
XX
XX Query Match 87.5%; Score 475; DB 2; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 8.5e-29;
XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
XX Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
XX Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQGVPSRF 60
XX
XX Qy 61 SGSGYGTDFLTITSSLPQDFASYYCOESLSASVTFGGQTKVEIKR 106
XX Db 61 SGSGYGTDFLTITSSLPQDFATYYCQSYSTPTTFGGQTKLEIKR 106
XX
XX RESULT 4
XX AAY98244
XX ID AAY98244 standard; protein; 107 AA.
XX AC AAY98244;
XX
XX 04-JUL-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX
XX Homo sapiens.
XX
XX AU9948754-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX
XX WPI; 2000-246867/22.
XX
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX
XX Example 9; Fig 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX (which does not comprise the sequence represented by AAY98206) and a
XX second polynucleotide encoding a light chain immunoglobulin amino acid
XX sequence; (b) inserting the first and second polynucleotide sequences
XX into a host cell; (c) maintaining the host cell in conditions which allow
XX the amino acid sequences encoded by the polynucleotides to be expressed
XX in the host cell; and (d) isolating the antibody comprising the heavy and
XX light chain immunoglobulin amino acid sequences from the host cell. The
XX anti-HIV gp-120 monoclonal antibody is used for providing passive
XX immunotherapy to HIV in a human. They can be administered to high-risk
XX patients to reduce the likelihood and/or severity of HIV-induced disease
XX and to patients who are already HIV-infected. The antibodies are used for
XX neutralising field isolates which provides information about the
XX immunocompetence of an immune response in HIV patients, for detecting HIV
XX in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX producing anti-idiotypic antibodies which can be used for active
XX immunisation and to screen human monoclonal antibodies to identify those
XX with the same binding specificity and to monitor the course of HIV
XX disease therapy by measuring the changes in concentration of HIV present
XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX monoclonal antibodies are encoded by a human polynucleotide sequence and
XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX reduce the problems of significant host immune response to the antibodies
XX associated with monoclonal antibodies of xenogeneic or chimeric
XX derivation
XX
XX Sequence 107 AA;
XX
XX Query Match 87.5%; Score 475; DB 3; Length 107;
XX Best Local Similarity 87.7%; Pred. No. 8.5e-29;
XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
XX Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
XX Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQGVPSRF 60
XX
XX Qy 61 SGSGYGTDFLTITSSLPQDFASYYCOESLSASVTFGGQTKVEIKR 106
XX Db 61 SGSGYGTDFLTITSSLPQDFATYYCQSYSTPTTFGGQTKLEIKR 106
XX
XX RESULT 5
XX AAY95135
XX ID AAY95135 standard; protein; 107 AA.
XX AC AAY95135;
XX
XX 30-JUN-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
XX Homo sapiens.
XX
XX AU9948756-A.
XX

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XX 17-FEB-2000.  
 XX 16-SEP-1999; 99AU-00048756.  
 XX 16-SEP-1999; 99AU-00048756.  
 XX (SRI ) SCRIPS RES INST.  
 XX Burton DR, Barbas CF, Lerner RA;  
 XX WPI: 2000-293393/26.  
 XX Novel human monoclonal antibodies which immunoreact with and neutralize  
 XX human immunodeficiency virus useful for treating HIV infections.  
 XX Example 9; Fig 11; 366pp; English.  
 XX The present sequence represents a fragment of an anti-human  
 XX immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
 XX a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
 XX mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
 XX gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
 XX in vitro virus infectivity assay by 50%, at a concentration of less than  
 XX 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
 XX immunotherapy of HIV induced disease. They are useful as neutralising  
 XX field isolates and provide useful information regarding the  
 XX immunocompetence of an immune response in HIV infected patients. The  
 XX monoclonal antibodies are useful for producing anti-idiotypic antibodies  
 XX which can be used to screen human monoclonal antibodies to identify  
 XX whether the antibody has the same binding specificity as the antibodies  
 XX of the invention. The neutralising antibodies define new epitopes on the  
 XX HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
 XX monoclonal antibodies derives from the fact that they are encoded by a  
 XX human polynucleotide sequence. Thus in vivo use of the monoclonal  
 XX antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
 XX reduces the problems of significant host immune response to the passively  
 XX administered antibodies which is a problem commonly encountered when  
 XX monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
 XX An additional major advantage of the monoclonal antibodies described  
 XX derives from the fact that they immunoreact with a unique determinant  
 XX present on mature HIV glycoprotein gp120. This class of antibodies is  
 XX particularly effective at neutralising field isolates of HIV  
 XX Sequence 107 AA;  
 XX Query Match 87.5%; Score 475; DB 3; Length 107;  
 XX Best Local Similarity 87.7%; Pred. No. 8.5e-29;  
 XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
 QY 61 SSGSGYGTDFTLTISSLOQFEDFASYCOESLSASYTFGQGTKEIKR 106  
 DB 61 SSGSGYGTDFTLTISSLOQFEDFATYCCQSYSTPTFTFGQGTKEIKR 106  
 RESULT 6  
 AAG93667  
 ID AAG93667 standard; protein; 107 AA.  
 XX AAG93667;  
 XX 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) antibody clone SH54 protein sequence.  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 XX red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX

OS Homo sapiens.  
 XX US62555455-B1.  
 XX 03-JUL-2001.  
 XX 29-JAN-1999; 99US-00240274.  
 XX 11-OCT-1996; 96US-0028550P.  
 XX 27-JUN-1997; 97US-00884045.  
 XX 10-APR-1998; 98US-0081380P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel DL;  
 XX WPI: 2001-388931/41.  
 XX N-PSDB; AAH68724.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 XX diagnostics requiring a human instead of an animal antibody and in  
 XX therapeutic medicine.  
 XX Claim 1; Col 70; 162pp; English.  
 XX The present invention describes an isolated Rh(D) binding protein,  
 XX preferably a human antibody, (I) having an amino acid sequence comprising  
 XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 XX immunostimulant activity, and can be used as an immune system stimulant.  
 XX (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 XX are used in diagnostics that require human antibodies instead of animal  
 XX antibodies, such as determine the Rh phenotype of human red blood cells.  
 XX AAG8615 to AAH68726 represent the nucleotide sequence which encode  
 XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 XX chain CDR3 amino acid sequences which are given in the exemplification of  
 XX the present invention  
 XX Sequence 107 AA;  
 XX Query Match 87.3%; Score 474; DB 4; Length 107;  
 XX Best Local Similarity 87.7%; Pred. No. 1e-28;  
 XX Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61  
 QY 61 SSGSGYGTDFTLTISSLOQFEDFASYCOESLSASYTFGQGTKEIKR 106  
 DB 62 SSGSGYGTDFTLTISSLOQFEDFATYCCQSYSTPTFTFGQGTKEIKR 107  
 RESULT 7  
 ABO27474  
 ID ABO27474 standard; protein; 107 AA.  
 XX ABO27474;  
 XX 12-SEP-2003 (first entry)  
 XX Anti-Rh(D) light chain SH54.  
 XX Human; RH(D) binding protein; blood typing; blood product; antibody;  
 XX magnetically activated cell sorting.  
 XX Homo sapiens.  
 XX US2003040605-A1.  
 XX 27-FEB-2003.  
 XX 04-MAY-2001; 2001US-00848798.  
 XX



PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 FA Siegel DL;  
 XX WPI; 2001-388931/41.  
 XX N-PSDB; ACD45388.  
 DR New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 PT Claim 4; Page 53; 187pp; English.  
 PS The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX Sequence 107 AA;  
 SQ Query Match 87.3%; Score 474; DB 6; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1e-28;  
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 ELTQSPSSLSASVGDRTVITCRASQRTINTYLNWYQHKFGKAPKLLIYAASSLQSGVPSRF 60  
 Db 2 ELTQSPSSMSASVGDRTVITCRASQRTIGTYLNWYQKFGKAPKLLIYAASSLQSGVPSRF 61  
 Qy 61 SGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTGKVEIKR 106  
 Db 62 SGSGGTDFLTITSSLOFEDFATYCOQSYSTPTWTFQGTGKVEIKR 107  
 RESULT 8  
 AAG93663  
 ID AAG93663 standard; protein; 107 AA.  
 XX AC AAG93663;  
 XX 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) antibody clone SH49 protein sequence.  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 XX red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX Homo sapiens.  
 XX US6255455-B1.  
 XX 03-JUL-2001.  
 XX 29-JAN-1999; 99US-00240274.  
 XX 11-OCT-1996; 96US-0028550P.  
 XX 27-JUN-1997; 97US-00884045.  
 XX 10-APR-1998; 98US-0081380P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel DL;  
 XX WPI; 2001-388931/41.  
 XX N-PSDB; AAG68720.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.

XX Claim 1; Col 69; 162pp; English.  
 PS The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 XX Sequence 107 AA;  
 SQ Query Match 86.9%; Score 472; DB 4; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.4e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 ELTQSPSSLSASVGDRTVITCRASQRTINTYLNWYQHKFGKAPKLLIYAASSLQSGVPSRF 60  
 Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISSYLNWYQKFGKAPKLLIYAASSLQSGVPSRF 61  
 Qy 61 SGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTGKVEIKR 106  
 Db 62 SGSGGTDFLTITSSLOFEDFATYCOQSYSTPTWTFQGTGKVEIKR 107  
 RESULT 9  
 AAG93664  
 ID AAG93664 standard; protein; 107 AA.  
 XX AC AAG93664;  
 XX 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) antibody clone SH50 protein sequence.  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 XX red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX Homo sapiens.  
 XX US6255455-B1.  
 XX 03-JUL-2001.  
 XX 29-JAN-1999; 99US-00240274.  
 XX 11-OCT-1996; 96US-0028550P.  
 XX 27-JUN-1997; 97US-00884045.  
 XX 10-APR-1998; 98US-0081380P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel DL;  
 XX WPI; 2001-388931/41.  
 XX N-PSDB; AAH68721.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX Claim 1; Col 69; 162pp; English.  
 PS The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.4e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61  
 QY 61 SGSGYGTDFTLTISSLPQDFASYCQESLSASYTFGQGTKEIKR 106  
 DB 62 SGSGGTDFTLTISSLPQDFATYYCQSQSYSTFWTFGQGTKEIKR 107

RESULT 10  
 AAG93590  
 ID AAG93590 standard; protein; 107 AA.

AC AAG93590;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) chain I02 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US625545-51-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2001-388931/41.

DR N-PSDB; AAH68647.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.

PS Claim 1; Col 43, 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.4e-28;  
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SGSGYGTDFTLTISSLPQDFASYCQESLSASYTFGQGTKEIKR 106

DB 62 SGSGGTDFTLTISSLPQDFATYYCQSQSYSTFWTFGQGTKEIKR 107

RESULT 11

ABO27471  
 ID ABO27471 standard; protein; 107 AA.

XX ABO27471;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH50.

KW Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KW magnetically activated cell sorting.

OS Homo sapiens.

XX US2003040605-A1.

PN 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2003-512273/48.

DR N-PSDB; ACD45385.

XX New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.

PS Claim 4; Page 52; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain

SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.4e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

DB 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SGSGYGTDFTLTISSLPQDFASYCQESLSASYTFGQGTKEIKR 106

DB 62 SGSGGTDFTLTISSLPQDFATYYCQSQSYSTFWTFGQGTKEIKR 107

## RESULT 12

ABO27397  
 ID ABO27397 standard; protein; 107 AA.  
 XX  
 AC ABO27397;  
 XX  
 DT 12-SEP-2003 (first entry)  
 XX  
 DE Anti-Rh(D) chain I02.  
 XX  
 KW Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KW magnetically activated cell sorting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003040605-A1.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 04-MAY-2001; 2001US-00848798.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2003-512273/48.  
 DR N-PSDB; ACD45311.  
 XX  
 PT New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX  
 PS Claim 4; Page 26; 187pp; English.  
 XX  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX  
 SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 1.4e-28;  
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINWYQHKPGKAPKLLIYAASSLQSGVPSRF 60  
 Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINWYQHKPGKAPKLLIYAASSLQSGVPSRF 61  
 QY 61 SGSGYGDFTLTITSSLOFEDFASVYCOESLSASVTFQGGTKVEIKR 106  
 Db 62 SGSGSGDFTLTITSSLOFEDFATYCCQSYSTLWTFQGGTKVEIKR 107

## RESULT 13

ABO27470  
 ID ABO27470 standard; protein; 107 AA.  
 XX  
 AC ABO27470;  
 XX  
 DT 12-SEP-2003 (first entry)  
 XX  
 DE Anti-Rh(D) light chain SH49.  
 XX  
 KW Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KW magnetically activated cell sorting.  
 XX  
 OS Homo sapiens.

XX US2003040505-A1.  
 PN 27-FEB-2003.  
 XX  
 PD 04-MAY-2001; 2001US-00848798.  
 XX  
 PF 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2003-512273/48.  
 DR N-PSDB; ACD45384.  
 XX  
 PT New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX  
 PS Claim 4; Page 52; 187pp; English.  
 XX  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX  
 SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 1.4e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINWYQHKPGKAPKLLIYAASSLQSGVPSRF 60  
 Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINWYQHKPGKAPKLLIYAASSLQSGVPSRF 61  
 QY 61 SGSGYGDFTLTITSSLOFEDFASVYCOESLSASVTFQGGTKVEIKR 106  
 Db 62 SGSGSGDFTLTITSSLOFEDFATYCCQSYSTWTFQGGTKVEIKR 107

## RESULT 14

AAG93644  
 ID AAG93644 standard; protein; 107 AA.  
 XX  
 AC AAG93644;  
 XX  
 DT 14-SEP-2001 (first entry)  
 XX  
 DE Human anti-Rh(D) antibody clone SH13 protein sequence.  
 XX  
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6255455-B1.  
 XX  
 PD 03-JUL-2001.  
 XX  
 PF 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;

XX WPI; 2001-388931/41.  
DR N-PSDB; AAH68701.  
XX  
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX  
XX Claim 1; Col 68; 162pp; English.  
PS  
XX The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93658 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. CC AAH68615 to AAH68726 represent the nucleotide sequence which encode CC AAG93658 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of CC the present invention  
XX  
XX Sequence 107 AA;  
SQ

Query Match 86.7%; Score 471; DB 4; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.7e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60  
DB 2 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 61  
QY 61 SGSGYGTDTLTITSSLPQEDFASYCQESLSASYTFGGQTKVEIKR 106  
DB 62 SGSGGTDTLTITSSLPQEDFATYCCQSYSTPYTFGGQTKLEIKR 107

RESULT 15  
ABO27451  
ID ABO27451 standard; protein; 107 AA.  
XX  
AC ABO27451;  
DT  
DT 12-SEP-2003 (first entry)  
XX  
DE Anti-Rh(D) light chain SH13.  
XX  
KW Human; RH(D) binding protein; blood typing; blood product; antibody;  
KW magnetically activated cell sorting.  
XX  
OS Homo sapiens.  
XX  
PN US2003040605-A1.  
XX  
PD 27-FEB-2003.  
XX  
PF 04-MAY-2001; 2001US-00848798.  
XX  
PR 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-00884045.  
PR 10-APR-1998; 98US-0081380P.  
PR 29-JAN-1999; 99US-00240274.  
XX  
FA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Siegel DL;  
XX  
XX WPI; 2003-512273/48.  
DR N-PSDB; ACD45365.  
XX  
XX New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
PT  
XX

PS Claim 4; Page 50; 187pp; English.  
XX  
CC The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents the amino acid sequence of a human anti-Rh(D) chain  
XX  
SQ Sequence 107 AA;  
Query Match 86.7%; Score 471; DB 6; Length 107;  
Best Local Similarity 86.8%; Pred. No. 1.7e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60  
DB 2 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 61  
QY 61 SGSGYGTDTLTITSSLPQEDFASYCQESLSASYTFGGQTKVEIKR 106  
DB 62 SGSGGTDTLTITSSLPQEDFATYCCQSYSTPYTFGGQTKLEIKR 107  
Search completed: August 8, 2004, 12:13:48  
Job time : 45.5242 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 35.8152 Seconds  
(without alignments)  
928.389 Million cell updates/sec

Title: US-10-027-725A-10  
Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	100.0	106	14	US-10-027-725A-10
2	475	87.5	107	14	US-10-016-986-104
3	474	87.3	107	10	US-09-848-798-179
4	472	86.9	107	10	US-09-848-798-33
5	472	86.9	107	10	US-09-848-798-175
6	472	86.9	107	10	US-09-848-798-176
7	471	86.7	107	10	US-09-848-798-156
8	468	86.2	107	10	US-09-848-798-36
9	467	86.0	107	14	US-10-016-986-105
10	465	85.6	111	14	US-10-203-754A-57
11	464.5	85.5	108	10	US-09-848-798-32
12	464.5	85.5	108	10	US-09-848-798-43
13	464	85.5	107	10	US-09-848-798-37
14	464	85.5	240	9	US-09-192-854-2
15	464	85.5	240	9	US-09-968-561A-2

16	454	85.5	240	10	US-09-968-744A-2
17	454	85.5	240	12	US-09-968-561A-2
18	463	85.3	107	10	US-09-791-153A-67
19	462	85.1	106	14	US-10-027-725A-12
20	462	85.1	107	10	US-09-848-798-38
21	462	85.1	107	10	US-09-848-798-39
22	461	84.9	107	10	US-09-848-798-158
23	460.5	84.8	108	10	US-09-848-798-167
24	460	84.7	106	14	US-10-027-725A-11
25	459.5	84.6	108	10	US-09-848-798-163
26	458	84.3	107	10	US-09-848-798-35
27	458	84.3	107	10	US-09-848-798-173
28	458	84.3	111	14	US-10-203-754A-56
29	457	84.2	104	14	US-10-016-986-106
30	457	84.2	107	10	US-09-848-798-40
31	457	84.2	214	14	US-10-153-382-19
32	456	84.0	107	10	US-09-848-798-44
33	455	83.8	107	15	US-10-309-762-88
34	454.5	83.7	107	12	US-10-363-349-4
35	454.5	83.7	288	12	US-10-363-349-7
36	454	83.6	233	16	US-10-663-244-150
37	452	83.2	107	10	US-09-848-798-172
38	452	83.2	107	10	US-09-848-798-174
39	452	83.2	107	16	US-10-723-434-40
40	452	83.2	291	12	US-10-406-830-10
41	451.5	83.1	108	10	US-09-848-798-41
42	451.5	83.1	108	14	US-10-016-986-109
43	451	83.1	107	10	US-09-848-798-168
44	451	83.1	107	15	US-10-309-762-89
45	451	83.1	108	12	US-10-371-942-8

#### ALIGNMENTS

##### RESULT 1

US-10-027-725A-10  
; Sequence 10, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-10

Query Match 100.0%; Score 543; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.7e-43;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGDRTVTSICRASORINLYNWYQHKGKAPKLLIYAASSLSQGVPSRF 60

Db 1 ELTQSPSSLSASVGDRTVTSICRASORINLYNWYQHKGKAPKLLIYAASSLSQGVPSRF 60

OY 61 SGSGYGTDTLTITSSLFQDFASYYCQESLSASYTFGGTKVEIKR 106

Db 61 SGSGYGTDTLTITSSLFQDFASYYCQESLSASYTFGGTKVEIKR 106

##### RESULT 2

US-10-016-986-104  
; Sequence 104, Application US/10016986  
; Publication No. US20030187247A1  
; GENERAL INFORMATION:

```

; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      87.5%; Score 475; DB 14; Length 107;
Best Local Similarity 87.7%; Pred. No. 4.1e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
QY 61 SSGSGYGTDFTLTISSLOFDFASYCOESLSASYTFGGTKVEIKR 106
Db 61 SSGSGYGTDFTLTISSLOFDFASYCOESLSASYTFGGTKVEIKR 106

RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match      87.3%; Score 474; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 5e-37;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60

```

```

; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.8e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SSGSGYGTDFTLTISSLOFDFASYCOESLSASYTFGGTKVEIKR 106
Db 62 SSGSGYGTDFTLTISSLOFDFASYCOESLSASYTFGGTKVEIKR 107

RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 7.8e-37;

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; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match      86.0%; Score 467; DB 14; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-36;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDVRTTISCRASQRIINTVLNMYQHKPGKAPKLLIYAASSLQSGVPSRF 60
DB      1 ELTQSPSSLSASVGDVRTTITCRASQSISSVLNMYQQKPGKAPKLLIYAASSLQSGVPSRF 60

QY      61 SGSGYGTDTFTLTISLQFEDFASYYCQESLSASYTEGQGTKEIKR 106
DB      61 SGSGSGTDTFTLTISLQPEDFATYYCQSYSTPTQTEGQGTKEIKR 106

RESULT 10
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-754A-57

Query Match      85.6%; Score 465; DB 14; Length 111;
Best Local Similarity 84.8%; Pred. No. 3.7e-36;
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY      2 LTQSPSSLSASVGDVRTTISCRASQRIINTVLNMYQHKPGKAPKLLIYAASSLQSGVPSRFS 61
DB      4 MTQSPSSLSASVGDVRTTITCRASQISNLNMYQQKPGKAPKLLIYAASSLQSGVPSRFS 63

QY      62 GSGYGTDTFTLTISLQFEDFASYYCQESLSASYTEGQGTKEIKR 106
DB      64 GSGSGTDTFTLTISLQPEDFATYYCQSYTPTPTTEGQGTKEIKR 108

RESULT 11
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: SPOTTING METHOD FOR PRODUCTION THEREOF

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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37
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Query Match      85.5%; Score 464; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 4.4e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SGSGYGTDFTLTISSLOPEDFASYCOESLSASVTFGGTKVEIKR 106
Db 62 SGSGGTDFTLTISSLOPEDFATYCCQSYSTPTTFGGTKRLIKR 107
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## RESULT 14

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US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. US20020068276A1
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; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2
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Query Match      85.5%; Score 464; DB 9; Length 240;
Best Local Similarity 85.8%; Pred. No. 1e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 135 QMTQSPSSLSASVGDVRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 194

QY 61 SGSGYGTDFTLTISSLOPEDFASYCOESLSASVTFGGTKVEIKR 106
Db 195 SGSGGTDFTLTISSLOPEDFATYCCQSYSTPTTFGGTKVEIKR 240
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## RESULT 15

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US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US20020164642A1
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; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
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; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2
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Query Match      85.5%; Score 464; DB 9; Length 240;
Best Local Similarity 85.8%; Pred. No. 1e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRTVITCRASQRIINTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 135 QMTQSPSSLSASVGDVRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 194

QY 61 SGSGYGTDFTLTISSLOPEDFASYCOESLSASVTFGGTKVEIKR 106
Db 195 SGSGGTDFTLTISSLOPEDFATYCCQSYSTPTTFGGTKVEIKR 240
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Search completed: August 8, 2004, 12:43:21
Job time : 36.8152 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 12.6879 Seconds  
(without alignments)  
431.306 Million cell updates/sec

Title: US-10-027-725A-10  
Perfect score: 543  
Sequence: 1 ELTQSPSSLASVGDRTVIS.....QESLSASYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	87.5	107	US-08-276-852-104	Sequence 104, App
2	475	87.5	107	US-08-899-575-104	Sequence 104, App
3	475	87.5	107	US-08-899-575-104	Sequence 104, App
4	475	87.5	107	PCT-US95-08743-104	Sequence 104, App
5	474	87.3	107	US-09-240-274-179	Sequence 179, App
6	472	86.9	107	US-09-240-274-33	Sequence 33, App
7	472	86.9	107	US-09-240-274-175	Sequence 175, App
8	472	86.9	107	US-09-240-274-176	Sequence 176, App
9	471	86.7	107	US-09-240-274-156	Sequence 156, App
10	468	86.2	107	US-09-240-274-36	Sequence 36, App
11	467	86.0	107	US-08-276-852-105	Sequence 105, App
12	467	86.0	107	US-08-899-575-105	Sequence 105, App
13	467	86.0	107	US-08-899-575-105	Sequence 105, App
14	467	86.0	107	PCT-US95-08743-105	Sequence 105, App
15	464.5	85.5	108	US-09-240-274-32	Sequence 32, App
16	464.5	85.5	108	US-09-240-274-43	Sequence 43, App
17	464	85.5	107	US-09-240-274-37	Sequence 37, App
18	462	85.1	107	US-09-240-274-38	Sequence 38, App
19	462	85.1	107	US-09-240-274-39	Sequence 39, App
20	461	84.9	107	US-09-240-274-158	Sequence 158, App
21	460.5	84.8	108	US-09-240-274-167	Sequence 167, App
22	459.5	84.6	108	US-09-240-274-163	Sequence 163, App
23	458	84.3	107	US-09-240-274-35	Sequence 35, App
24	458	84.3	107	US-09-240-274-173	Sequence 173, App
25	458	84.3	108	US-08-379-057-29	Sequence 29, App
26	457	84.2	104	US-08-276-852-106	Sequence 106, App
27	457	84.2	104	US-08-899-575-106	Sequence 106, App

## ALIGNMENTS

RESULT 1  
US-08-276-852-104  
; Sequence 104, Application US/08276852  
; Patent No. 5652138  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/276,852  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRL452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-276-852-104

28 457 84.2 104 1 US-08-899-575-106 Sequence 106, App  
29 457 84.2 104 5 PCT-US95-08743-106 Sequence 106, App  
30 457 84.2 107 3 US-09-240-274-40 Sequence 40, Appl  
31 457 84.2 214 4 US-09-472-087-71 Sequence 71, Appl  
32 456 84.0 107 3 US-09-240-274-44 Sequence 44, Appl  
33 452 83.2 107 3 US-09-240-274-172 Sequence 172, App  
34 452 83.2 107 3 US-09-240-274-174 Sequence 174, App  
35 451.5 83.1 108 1 US-08-276-852-109 Sequence 109, App  
36 451.5 83.1 108 1 US-08-899-575-109 Sequence 109, App  
37 451.5 83.1 108 3 US-08-899-575-109 Sequence 109, App  
38 451.5 83.1 108 3 US-09-240-274-41 Sequence 41, Appl  
39 451.5 83.1 108 5 PCT-US95-08743-109 Sequence 109, App  
40 451 83.1 107 3 US-09-240-274-168 Sequence 168, App  
41 451 83.1 108 4 US-09-025-769B-14 Sequence 14, Appl  
42 451 83.1 109 2 US-07-934-373C-3 Sequence 3, Appl  
43 451 83.1 109 3 US-08-437-642B-3 Sequence 3, Appl  
44 451 83.1 109 4 US-08-146-206C-3 Sequence 3, Appl  
45 451 83.1 109 4 US-09-705-686-3 Sequence 3, Appl

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 9.5e-39;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFQGTQKVEIKR 106  
Db 61 SGSGGTDFLTITSSLOPEDFATYCCQSYSTPTPTFGQGTQKLEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 9.5e-39;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFQGTQKVEIKR 106  
Db 61 SGSGGTDFLTITSSLOPEDFATYCCQSYSTPTPTFGQGTQKLEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 9.5e-39;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60  
QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFQGTQKVEIKR 106  
Db 61 SGSGGTDFLTITSSLOPEDFATYCCQSYSTPTPTFGQGTQKLEIKR 106

RESULT 4  
PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743

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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      87.5%; Score 475; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.5e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||

QY 61 SGSGYGTDFLTITSSLOPDEFASYCQESLSASVTFGGTKVEIKR 106
   |||||
Db 61 SGSGGTDFLTITSSLOPDEFATYCCQSYSTPTVTFGGTKVEIKR 106
   |||||

RESULT 5
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.2e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSMSASVGDRTVITCRASQRTIGTLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||

QY 61 SGSGYGTDFLTITSSLOPDEFASYCQESLSASVTFGGTKVEIKR 106
   |||||
Db 62 SGSGGTDFLTITSSLOPDEFATYCCQSYSTPTVTFGGTKVEIKR 107
   |||||

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISYLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISYLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||
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RESULT 6
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.8e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISYLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||

QY 61 SGSGYGTDFLTITSSLOPDEFASYCQESLSASVTFGGTKVEIKR 106
   |||||
Db 62 SGSGGTDFLTITSSLOPDEFATYCCQSYSTLTWTFGGTKVEIKR 107
   |||||
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RESULT 7
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRTINLYNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
   |||||
Db 2 ELTQSPSSLSASVGDRTVITCRASQRTISYLYNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
   |||||
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QY 61 SGSGYGTDTLTITSSLOFEDFASYCOESLSASYSYTFGQGTKEIKR 106
DB 62 SGSGGTDFTLTITSSLOPEDFATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 8
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match 86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQIRYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQIRYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SGSGYGTDTLTITSSLOFEDFASYCOESLSASYSYTFGQGTKEIKR 106
DB 62 SGSGGTDFTLTITSSLOPEDFATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 9
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match 86.7%; Score 471; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQIRYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQIRYLNWYQKPKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SGSGYGTDTLTITSSLOFEDFASYCOESLSASYSYTFGQGTKEIKR 106
DB 62 SGSGGTDFTLTITSSLOPEDFATYYCQSYSTPTWTFGQGTKEIKR 107

RESULT 11
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
```

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/ FILING DATE: 18-JUL-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/178,302
/ FILING DATE: 30-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/954,148
/ FILING DATE: 30-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR1452P
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 105:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-276-852-105

Query Match 86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLSASVGDRTVITCRASQRIINYNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 1 ELTQSPSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFGGTKVEIKR 106
Db 61 SGSGYGTDFLTITSSLOFEDFATYYCQSYSTPQTGGTKLEIKR 106

RESULT 12
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
```

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR1452P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 105:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLSASVGDRTVITCRASQRIINYNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
Db 1 ELTQSPSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFGGTKVEIKR 106
Db 61 SGSGYGTDFLTITSSLOFEDFATYYCQSYSTPQTGGTKLEIKR 106

RESULT 13
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop IPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-105

Query Match      86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASORINTYLNWYQHKGKAPKLLIYAASSLSQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
QY 61 SGSGYGTDFTLTISSLPQEDFASYVCQESLSASYSYTFQGGTKVEIKR 106
DB 61 SGSGSGTDFTLTISSLPQEDFATYYCQOSYSTPTPQTFQGGTKLEIKR 106

RESULT 14
PCT-US95-08743-105
; Sequence 105, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match      86.0%; Score 467; DB 5; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.6e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASORINTYLNWYQHKGKAPKLLIYAASSLSQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
QY 61 SGSGYGTDFTLTISSLPQEDFASYVCQESLSASYSYTFQGGTKVEIKR 106
DB 61 SGSGSGTDFTLTISSLPQEDFATYYCQOSYSTPTPQTFQGGTKLEIKR 106

RESULT 15
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

```
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32

Query Match      85.5%; Score 464.5; DB 3; Length 108;
Best Local Similarity 86.9%; Pred. No. 9.8e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASORINTYLNWYQHKGKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SGSGYGTDFTLTISSLPQEDFASYVCQESLSA-SYTFQGGTKVEIKR 106
DB 62 SGSGSGTDFTLTISSLPQEDFATYYCQOSYSTPTPQTFQGGTKLEIKR 108

Search completed: August 8, 2004, 12:20:24
Job time : 12.6879 secs
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 9.31515 Seconds  
(without alignments)  
1094.593 Million cell updates/sec

Title: US-10-027-725A-11  
 Perfect score: 547  
 Sequence: 1 ELTQSPSSLSASVGDRVIT.....QQSYTYTFSGTGKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database : PIR 78:**
1:  _pir1:**
2:  _pir2:**
3:  _pir3:**
4:  _pir4:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	468	85.6	108	2	B49047	Ig kappa chain V r	
2	465	85.0	108	2	S47182	Ig kappa chain - h	
3	465	85.0	127	2	S47067	Ig kappa chain V-J	
4	464	84.8	109	2	S31998	Ig kappa chain - h	
5	462	84.5	123	2	S40331	Ig kappa chain - h	
6	457	83.5	122	2	S40370	Ig kappa chain - h	
7	455	83.2	108	2	S44122	Ig kappa chain V r	
8	454	83.0	108	2	S31977	Ig kappa chain - h	
9	453	82.8	129	1	K1HUWK	Ig kappa chain - h	
10	451	82.4	109	2	S31981	Ig kappa chain pre	
11	451	82.4	109	2	S31978	Ig kappa chain - h	
12	449	82.1	108	1	K1HUDE	Ig kappa chain - h	
13	447	81.7	108	2	S19674	Ig kappa chain - h	
14	446	81.5	129	2	S40317	Ig kappa chain V-I	
15	438	80.1	117	2	S46371	Ig kappa chain V r	
16	437.5	80.0	106	2	P2397	Ig kappa chain - h	
17	437	79.9	107	2	S36264	anti-tetanus toxin	
18	437	79.9	108	1	K1HUHU	Ig lambda chain V	
19	437	79.9	120	2	S46370	Ig kappa chain V-I	
20	436	79.7	109	2	S31979	Ig kappa chain V-J	
21	434	79.3	129	2	S52793	Ig kappa chain - h	
22	433	79.2	128	2	S46372	Ig kappa chain V r	
23	432	79.0	109	2	S31980	Ig light chain var	
24	432	79.0	125	2	S40350	Ig kappa chain - h	
25	431	78.8	109	2	S31983	Ig kappa chain - h	
26	429	78.4	129	2	S52792	Ig kappa chain - h	
27	429	78.4	132	2	S40334	Ig kappa chain V r	
28	428	78.2	109	2	S32001	Ig kappa chain - h	
29	428	78.2	122	2	S40314	Ig kappa chain - h	

## ALIGNMENTS

RESULT 1  
B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (frag  
 C; Species: Homo sapiens (man)  
 C; Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C; Accession: B49047  
 R; Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
 Eur. J. Immunol. 22, 2231-2236, 1992  
 A; Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
 A; Reference number: A49047; PMID:92387234; PMID:1516616

	Query Match	85.6%	Score 468;	DB 2;	Length 108;
	Best Local Similarity	84.9%;	Pred. No.	5.6e-36;	
	Matches	90;	Conservative	11; Mismatches	5; Indels    0; Gaps    0;
QY	1	EUTQSPPSLASVGDRTVTTCRAQISISTVLNNWQQKPGKAPKLIIWSASNLSQGVSRRF	60		
Db	:	:::::::::::::::::::::	:	:	:
3	QMTQSPSLSASVGDRVTITCRASQSISSYLNNWQQKPGKAPKLIIYAASLQSGVESRPF	62			
QY	61	SCSGSGTETLLIISNLQDFDFAYYCQSYTHLYTFGSGTKLEIKR	106		
Db	:	::::     :::     :	:	:	:
63	SCSGSGTDPTLISSLQPEDFAFYVCQSYSTPLTFGGGTKVIKR	108			

RESULT 2  
S47182

Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S47182  
 R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
 submitted to the EMBL Data Library, June 1994  
 A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patie  
 A:Reference number: S47181  
 A:Accession: S47182  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <MCI>  
 A:Cross-references: EMBL:X79786; NID:G506422; PID:CAA56182.1; PID:G506423  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 465; DB 2; Length 108;

62 GSGSGTEFTLTISNLQFEDFASYCQQSYTTLTYTFGSGTKLEIKR 106

C; Date: 13-Jan-1993  
C: Association: SA41722

A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into 12  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>  
F:23-45/Region: framework 1  
F:38-112/Domain: immunoglobulin homology <IMM>  
F:46-56/Region: complementarity-determining 1  
F:57-71/Region: framework 2  
F:72-78/Region: complementarity-determining 2  
F:79-110/Region: framework 3  
F:111-119/Region: complementarity-determining 3  
F:120-129/Region: framework 4  
F:145-110/Disulfide bonds: #status predicted

Query Match 82.8%; Score 453; DB 1; Length 129;  
Best Local Similarity 83.8%; Pred. No. 1.6e-34;  
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSLSASVGDRTVTTCRAGISITLWNWYQQKPGKAPKLLIWSASNLSQGVSRRF 60  
:  
Db 25 QMTQSPSLSASVGDRTVTTCRASQISNYLNWYQQKPGKAPKLLIYASSLSQGVTSRF 84  
: :

Qy 61 SGSGSGTEFTLTISNLQPEDFASYCCQSYYTLTYFGSGTKLEIK 105  
:  
Db 85 SGSGSGTDFTLTISLSLPEDSATYCCQSYSTLTITFGGTRLEIK 129  
: :

RESULT 10  
S31981  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations a  
A:Reference number: S31977  
A:Accession: S31981  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
C:Cross-references: EMBL:Z15077; NID:g38493; PIDN:CAA78786.1; PID:g38494  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;  
Best Local Similarity 82.9%; Pred. No. 2e-34;  
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSLSASVGDRTVTTCRAGISITLWNWYQQKPGKAPKLLIWSASNLSQGVSRRFS 61  
:  
Db 4 MTQSPSLSASVGDRTVTTCRASQDISRYLNWYQQKPGKAPKLLIHGASTLESQGVGRFS 63  
: :

Qy 62 GSQSGTEFTLTISNLQPEDFASYCCQSYYTLTYFGSGTKLEIKR 106  
:  
Db 64 GSGSGTDFTLTISLPEDATYCCQSYSTPPTFGGTRLEIKR 108  
: :

RESULT 11  
S31978  
Ig kappa chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31978  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations a

A;Reference number: S31977

A;Accession: S31978

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <POR>

A;Cross-references: EMBL:Z15074; NID:g38487; PIDN:CAA78783.1; PID:g38488

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;

Best Local Similarity 82.9%; Pred. No. 2e-34;

Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGRVITTCRASQISITLYLNWYQKPKAPKLLIWSASNLQSGVPSRFS 61

Db 4 MTQSPSSLSASVGRVITTCRTSQTISRYLNWYQIPGKAPKLLIFAASTLTQTVPSRFG 63

QY 62 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

Db 64 GSGSGTFTLTISTLQPDFAFYCQOSYTTPTFGGQTKLEIKR 108

#### RESULT 12

KIHUDE

Ig kappa chain V-I region (Dee) - human (tentative sequence)

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000

C;Accession: A01865

R;Milstein, C.P.; Deverson, E.V.

Biochem. J. 123, 945-958, 1971

A;Title: The amino acid sequence of a human kappa light chain.

A;Reference number: A01865; MUID:72053133; PMID:5124396

A;Accession: A01865

A;Molecule type: protein

A;Residues: 1-108 <ML>

A;Note: the C region of this chain as the Inv (3) marker

C;Genetics:

A;Gene: GDB:IGKV1

A;Cross-references: GDB:136264

A;Map position: 2p12-2p12

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;16-90/Domain: immunoglobulin homology <IMM>

F;23-88/Disulfide bonds: #status predicted

Query Match 82.1%; Score 449; DB 1; Length 108;

Best Local Similarity 80.2%; Pred. No. 3.1e-34;

Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRASQISITLYLNWYQKPKAPKLLIWSASNLQSGVPSRFP 60

Db 3 ZMTQSPSSLSASVGRVITTCRASQISITLYLNWYQKPKAPKLLIFAASLLKSGVPSRFP 62

QY 61 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

Db 63 GSGSGTFTLTISGLLPEDFAFYCQOSYTTPTFGGQTKVEMTR 108

#### RESULT 13

S19674

Ig kappa chain V region (clone alpha-TEL9) - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000

C;Accession: S19674

R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 591-597, 1991

A;Title: Hy-passing immunization. Human antibodies from V-gene libraries displayed on phage

A;Reference number: S19663; MUID:92085276; PMID:1748994

A;Accession: S19674

A;Molecule type: mRNA

A;Residues: 1-108 <MAR>

A;Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g1335386

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 447; DB 2; Length 108;

Best Local Similarity 83.8%; Pred. No. 4.7e-34;

Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGRVITTCRASQISITLYLNWYQKPKAPKLLIWSASNLQSGVPSRFS 61

Db 4 LTQSPSSLSASVGRVITTCRASQISITLYLNWYQKPKAPKLLIYAASTLQSGVPSRFS 63

QY 62 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIKR 106

Db 64 GSGSGTFTLTINSLOQEDFAFYCQQTNSFPLTFGGGQTKLEIKR 108

#### RESULT 14

S40317

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C;Accession: S40317

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40317

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KL>

A;Cross-references: EMBL:X72427; NID:g441322; PIDN:CAA51095.1; PID:g441323

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 446; DB 2; Length 129;

Best Local Similarity 81.0%; Pred. No. 6.9e-34;

Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRASQISITLYLNWYQKPKAPKLLIWSASNLQSGVPSRFP 60

Db 24 QMTQSPSSLSLSDRVITTCRASQISITLYLNWYQKPKAPKFLIYGASSLQSGVPSRFP 83

QY 61 GSGSGTFTLTISNLQFEDPASYYCQOSYTTLYTFGSGTKLEIK 105

Db 84 GSGSGTFTLTISLQPEDFAFYCQQTYSPTPTFGGQTKVEIK 128

#### RESULT 15

S46371

Ig kappa chain V-J region (T24-3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C;Accession: S46371; S38645

R;Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination

A;Reference number: S46369; MUID:94313975; PMID:8039491

A;Accession: S46371

A;Molecule type: mRNA

A;Residues: 1-117 <BEN>

A;Cross-references: EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PID:g415960

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;23-97/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 438; DB 2; Length 117;

Best Local Similarity 80.6%; Pred. No. 3.4e-33;

Matches 87; Conservative 10; Mismatches 9; Indels 2; Gaps 1;



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: August 8, 2004, 12:09:01 ; Search time 5.78182 Seconds  
(without alignments)  
954.620 Million cell updates/sec  
Title: US-10-027-725a-11  
Perfect score: 547  
Sequence: 1 ELTQSPSSLSASVGRVTIT.....QQSYTYLTFTSGGKLEIKR 106  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	82.8	129	1 KV1W HUMAN	P04431 homo sapien
2	449	82.1	108	1 KV1E HUMAN	P01597 homo sapien
3	437	79.9	108	1 KV1H HUMAN	P01600 homo sapien
4	424	77.5	108	1 KV1N HUMAN	P01606 homo sapien
5	416	76.1	108	1 KV1B HUMAN	P01594 homo sapien
6	416	76.1	108	1 KV1O HUMAN	P01607 homo sapien
7	413.5	75.6	107	1 KV1D HUMAN	P01596 homo sapien
8	412	75.3	129	1 KV1X HUMAN	P04432 homo sapien
9	411.5	75.2	109	1 KV1T HUMAN	P01612 homo sapien
10	411	75.1	108	1 KV1S HUMAN	P01611 homo sapien
11	408	74.6	108	1 KV1V HUMAN	P04430 homo sapien
12	407	74.4	108	1 KV1F HUMAN	P01598 homo sapien
13	403	73.7	108	1 KV1P HUMAN	P01608 homo sapien
14	402	73.5	108	1 KV1A HUMAN	P01593 homo sapien
15	402	73.5	108	1 KV1G HUMAN	P01599 homo sapien
16	401	73.3	108	1 KV1L HUMAN	P01604 homo sapien
17	401	73.3	108	1 KV1Y HUMAN	P01603 homo sapien
18	399	72.9	108	1 KV1R HUMAN	P01610 homo sapien
19	396	72.4	108	1 KV1C HUMAN	P01595 homo sapien
20	395	72.2	108	1 KV1M HUMAN	P01605 homo sapien
21	393	71.8	108	1 KV1K HUMAN	P01603 homo sapien
22	384	70.2	108	1 KV1Q HUMAN	P01609 homo sapien
23	384	70.2	108	1 KV5M MOUSE	P01646 mus musculus
24	383	70.0	117	1 KV1J HUMAN	P01602 homo sapien
25	377	68.9	117	1 KV1I HUMAN	P01601 homo sapien
26	375	68.6	108	1 KV5N MOUSE	P01647 mus musculus
27	374	68.4	108	1 KV5K MOUSE	P01644 mus musculus
28	373	68.2	108	1 KV5D MOUSE	P01636 mus musculus
29	372	68.0	108	1 KV5L MOUSE	P01645 mus musculus
30	372	68.0	108	1 KV5S MOUSE	P01652 mus musculus
31	372	68.0	114	1 KV4A HUMAN	P01625 homo sapien
32	371	67.8	108	1 KV5O MOUSE	P01648 mus musculus
33	371	67.8	111	1 KV3M MOUSE	P01665 mus musculus

34	370	67.6	111	1 KV3O MOUSE	P01667 mus musculus
35	368	67.3	111	1 KV3L MOUSE	P01664 mus musculus
36	367	67.1	108	1 KV5P MOUSE	P01649 mus musculus
37	366	66.9	111	1 KV3Q MOUSE	P01669 mus musculus
38	366	66.9	149	1 KV5A MOUSE	P01633 mus musculus
39	365	66.7	136	1 KV5B MOUSE	P01634 mus musculus
40	364.5	66.6	129	1 KV3J HUMAN	P18135 homo sapien
41	363	66.4	108	1 KV3U MOUSE	P01650 mus musculus
42	362	66.2	111	1 KV3H MOUSE	P01660 mus musculus
43	362	66.2	111	1 KV3N MOUSE	P01666 mus musculus
44	362	66.2	134	1 KV4C HUMAN	P06314 homo sapien
45	361	66.0	108	1 KV5U MOUSE	P04946 mus musculus

ALIGNMENTS

RESULT 1

KV1W\_HUMAN  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobbeck H.G., Combratio G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
CC -----  
DR EXBL; X00965; CAA25477.1; ALT\_TERM.  
DR PIR; A01883; KIHUWK.  
DR HGSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig\_1.  
DR SMART; SM00406; Igv\_1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 82.8%; Score 453; DB 1; Length 129;  
Best Local Similarity 83.8%; Pred. No. 1.2e-40;  
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; KIHUOU.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 4,7e-39;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIQSYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 QMTQSPSSLSASVGDRTVITTCRAQSIQSYLNWYQKPGKAPKLLIWAASLPSGVPSRF 62
QY 61 SSGSGGTFTLTISNQLQFEDFASYCQSYTTLTFTGSGTKLEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
63 SSGSGGTFTLTISNQLQFEDFASYCQSYTTLTFTGSGTKLEIKR 108

RESULT 4
KVH_HUMAN STANDARD; PRT; 108 AA.
ID_KVH_HUMAN
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains.";
RL Science 169:56-59 (1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.

```

```

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIQSYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
25 QMTQSPSSLSASVGDRTVITTCRAQSIQSYLNWYQKPGKAPKLLIWAASLQSGVTSRF 84
QY 61 SSGSGGTFTLTISNQLQFEDFASYCQSYTTLTFTGSGTKLEIK 105
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
85 SSGSGGTFTLTISNQLQFEDFASYCQSYTTLTFTGSGTKLEIK 129

RESULT 2
KVH_HUMAN STANDARD; PRT; 108 AA.
ID_KVH_HUMAN
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958 (1971).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01865; KIHUDE.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.6e-40;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIQSYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 ZMTQSPSSLSASVGDRTVITTCRAQSIQSYLNWYQKPGKAPKLLIWAASLQSGVPSRF 62
QY 61 SSGSGGTFTLTISNQLQFEDFASYCQSYTTLTFTGSGTKLEIKR 106
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
63 SSGSGGTFTLTISNQLQFEDFASYCQSYTTLTFTGSGTKLEIKR 108

RESULT 3
KVH_HUMAN STANDARD; PRT; 108 AA.
ID_KVH_HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).

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DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA424105827E CRC64;

Query Match 77.5%; Score 424; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 1.1e-37;
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDVRVITICRAQSISTYLNWYQQKPKAPKLLIWSASNLQSGVPSRF 60
Db :::::::::::::::::::::
3 QMTSPSLASVGDVRVITICRAQTSSILEWYZZKPKAPBLIIYAASBLHSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLOFEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db :::::::::::::::::::::
63 SGSGSGTEFTLTISLZPZBFATYCYZSYSSPTFTFGZGTLZIKR 108

RESULT 5
KV10 HUMAN
ID KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiehl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RX X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; KIHUAV.
DR PDB; 1JW5; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA424105827E CRC64;

Query Match 77.5%; Score 424; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 1.1e-37;
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDVRVITICRAQSISTYLNWYQQKPKAPKLLIWSASNLQSGVPSRF 60
Db :::::::::::::::::::::
3 QMTSPSLASVGDVRVITICRAQTSSILEWYZZKPKAPBLIIYAASBLHSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLOFEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db :::::::::::::::::::::
63 SGSGSGTEFTLTISLZPZBFATYCYZSYSSPTFTFGZGTLZIKR 108

RESULT 6
KV10 HUMAN
ID KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BWV; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

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DR SMART; SM00406; IGV; 1;
DR PROSITE; PS50835; IG_LIKE; 1;
DR Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 75.6%; Score 413.5; DB 1; Length 107;
Best Local Similarity 72.6%; Pred. No. 1.4e-36;
Matches 77; Conservative 20; Mismatches 8; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVNLWYQKPGKAPKXLLIWSASNLQSGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVAITTCRASQNISSWLAWYQKPGKAPKVLIVKSSLSGSGVPSRF 62
QY 61 SGSGSGTEFTLTISNLQFEDFASYVCOQSYTTLYTFSGSGTKLEIKR 106
DB 63 SGSGSGTDFLTITSLZLPBBFATYYCQ-YNTFTFGPGTKVDIKR 107

RESULT 8
KV1X HUMAN
ID_KV1X_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
AT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Daudi precursor.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrinato G., Zachau H.G.;
RT Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).

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or send an email to license@isb-sib.ch).
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EMBL; X00966; CAA25478.1; ALT_TERM.
PIR; A01884; K1HUD1.
HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

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Query Match      75.3%; Score 412; DB 1; Length 129;
Best Local Similarity 74.3%; Pred. No. 2.4e-36;
Matches 78; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 25 QMTQSPSSLSASVGRVITTCRAGNIINFLSWYQKPGKAPKLLIYAVSNLQGVPSRF 84

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTYTLTYFGSGTKLEIK 105
Db 85 SGSGSGTEFTLTISNLQFEDFATYICQYNNFSTFGGGTKVDNK 129

RESULT 9
KV1T HUMAN
ID KV1T HUMAN STANDARD; PRT; 109 AA.
AC P01612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region Mv.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=83081018; PubMed=6816713;
RA Eulitz M., Linke R.P.;
RT "Primary structure of the variable part of an amyloidogenic
RT Bence-Jones Protein (Mv). An unusual insertion in the third
RT hypervariable region of a human kappa-immunoglobulin light chain.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
CC FOUND.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01879; KIHUMV.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 98 FRAMEWORK-4.
FT DOMAIN 99 108 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11870 MW; B6ABF4515D55F5A0 CRC64;

Query Match      75.2%; Score 411.5; DB 1; Length 109;
Best Local Similarity 76.6%; Pred. No. 2.3e-36;
Matches 82; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGRVITTCRASQSDYLNWYQKPGKAPKLLIFDTSLQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTYTLTYFGSGTKLEIK 106
Db 63 SGSGSGTEFTLTISNLQFEDFATYICQYNNFSTFGGGTKVDIKR 109

RESULT 10
KV1S HUMAN
ID KV1S HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krsche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01877; KIHUWS.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match      75.1%; Score 411; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 2.5e-36;
Matches 79; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGRVITTCRASQSDYLNWYQKPGKAPKLLIYASNLQGVPSRF 62

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTYTLTYFGSGTKLEIK 106
Db 63 SGSGSGTEFTLTISNLQFEDFATYICQYNNFSTFGGGTKVDIKR 108

RESULT 11
KV1V HUMAN
ID KV1V HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=86174817; PubMed=3083240;
RA Dwyer F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";

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RL Mol. Immunol. 23:73-78 (1986).
DR PIR; A01878; KIHUBN.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
FT SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 74.6%; Score 408; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 5,2e-36;
Matches 79; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITCRASQISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 3 QLTQSPSLASVGDRTVITCRASQSYVYVAWFQOKPGKAPKSLIYDASTLQSGVPSNF 62

QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTYTLTYFGSGTKLEIKR 106
DB 63 TGSGSGTDFLTISLQPEDFATYCCQYNSPYTFGGQTKVQIKR 108

RESULT 12
KVLP HUMAN STANDARD; PRT; 108 AA.
ID KVLP HUMAN
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottleib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]_
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR HSP; P01607; IREU.
DR PIR; A90562; KIHUR.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
FT SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 74.4%; Score 407; DB 1; Length 108;
Best Local Similarity 74.3%; Pred. No. 6.6e-36;
Matches 78; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITCRASQISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQSINTLWLAQQKPGKAPKLLIWSASNLQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTYTLTYFGSGTKLEIK 105
DB 63 IGSGSGTEFTLTISLQPEDFATYCCQYNSDSKMFQGTKEVK 107

RESULT 13
KVLP HUMAN STANDARD; PRT; 108 AA.
ID KVLP HUMAN
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]_
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
RA (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.

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FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 73.7%; Score 403; DB 1; Length 108;
Best Local Similarity 72.6%; Pred. No. 1.7e-35;
Matches 77; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCASQDIFLNWYQKPGKAPKLLIYDASNLQSGVPSRF 62
QY 61 SGSGSGCTFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 63 SGTSGTDFTFITISLQPEDATYTCQDFNLTFFGGTKVDFKR 108

RESULT 14
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 73.5%; Score 402; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 2.2e-35;
Matches 79; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCASQDINHLNHWYQKPGKAPKLLIYDASNLQSGVPSRF 62
QY 61 SGSGSGCTFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 63 SGSGGCTDFTFITISLQPEDATYTCQYDTLPRIFGGTKLEIKR 108

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RESULT 15
KV1G_HUMAN
ID KV1G_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I."
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 73.5%; Score 402; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 2.2e-35;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLTWYQKPGKAPKELIYAASNLQSGVPSRF 62
QY 61 SGSGSGCTFTLTISNLQFEDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 63 SGSGAGCTFTLTISLQPEDFATYTCLOQNSYPSRFGQGTKEIKR 108

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Search completed: August 8, 2004, 12:14:32  
Job time : 5.78182 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 29.0697 Seconds  
(without alignments)  
1150.508 Million cell updates/sec

Title: US-10-027-725A-11  
Perfect score: 547  
Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSYTTLVTFGSGTKLRIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	85.4	108	4 Q9UL77	Q9ul77 homo sapien
2	465.5	85.1	107	4 Q96SA9	Q96sa9 homo sapien
3	448.5	82.0	107	4 Q9UL81	Q9ul81 homo sapien
4	423	77.3	234	4 Q7Z473	Q7z473 homo sapien
5	414	75.7	108	4 Q9UL70	Q9ul70 homo sapien
6	413	75.5	108	4 Q9UL79	Q9ul79 homo sapien
7	408	74.6	236	4 Q7Z3Y4	Q7z3y4 homo sapien
8	387	70.7	298	11 Q9QYF0	Q9qyf0 mus musculus
9	379	69.3	234	11 Q9LWFB	Q9lwfb mus musculus
10	374	68.4	116	4 Q96PF6	Q96pf6 homo sapien
11	374	68.4	234	11 Q9RO62	Q9ro62 mus musculus
12	373	68.2	109	11 Q920E6	Q920e6 mus musculus
13	371	67.8	108	4 Q9UL83	Q9ul83 homo sapien
14	368	67.3	214	11 Q9RIAS	Q9rias mus musculus
15	367	67.1	234	11 Q8VCP0	Q8vcp0 mus musculus
16	366	66.9	111	11 Q920E9	Q920e9 mus musculus

## ALIGNMENTS

## RESULT 1

Q9UL77  
ID Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
DE  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1; --  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 85.4%; Score 467; DB 4; Length 108;  
Best Local Similarity 84.0%; Pred. No. 2e-44;  
Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSIYSTYLNWYQQKFKAPKLIIWSASNLQSGVPSRF 60

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus." RT Clin. Immunol. Immunopathol. 87:184-192 (1998). DR ENBL; AF035033; AAD56269.1; -. DR HSP; P01607; IREI. DR InterPro; IPR007110; Ig-like. DR InterPro; IPR003596; Ig\_v. DR Pfam; PF00047; Ig; 1. DR SMART; SM00406; IGV; 1. DR PROSITE; PS00835; IG\_LIKE; 1. FT NON TER 107 107 FT NON TER 107 107 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64; Query Match 82.0%; Score 448.5; DB 4; Length 107; Best Local Similarity 82.1%; Pred. No. 2.3e-42; Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1; Qy 1 ELTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIYASNLQSGVPSRF 60 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIYASNLQSGVPSRF 62 Qy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTFGSGTKLEIKR 106 Db 63 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTFGSGTKLEIKR 107 RESULT 4 Q2473 PRELIMINARY; PRT; 234 AA. ID Q2473 AC Q2473; DT 01-OCT-2003 (TrEMBLrel. 25, Created) DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE Hypothetical protein. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. OX NCBI\_TaxID=9606; FN [1] SEQUENCE FROM N.A. RP TISSUE=Lung; RC MEDLINE=22388257; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., RA Jones S.J., Marra M.A.; Qy RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). RN [2] SEQUENCE FROM N.A. RP TISSUE=Lung; RC Strausberg R.; RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases. DR ENBL; BC056256; AAB56256.1; -. KW Hypothetical protein. SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64; Query Match 77.3%; Score 423; DB 4; Length 234;

Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIYASNLQSGVPSRF 62 Qy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTFGSGTKLEIKR 106 Db 63 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTFGSGTKLEIKR 108 RESULT 2 Q96SA9 PRELIMINARY; PRT; 107 AA. ID Q96SA9 AC Q96SA9; DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment). OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. OX NCBI\_TaxID=9606; FN [1] SEQUENCE FROM N.A. RP MEDLINE=98375893; PubMed=9712075; RA Addison E.E., Shikhan A.R., Ward K.E., Cunningham M.W.; RT "Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes." RT J. Immunol. 161:2020-2031 (1998). RL ENBL; U96396; AAB68785.1; -. DR PIR; B49047; B49047. DR PIR; S34083; S34083. DR PIR; S34086; S34086. DR InterPro; IPR007110; Ig-like. DR InterPro; IPR003596; Ig\_v. DR Pfam; PF00047; Ig; 1. DR SMART; SM00406; IGV; 1. DR PROSITE; PS00835; IG\_LIKE; 1. FT NON TER 1 1 FT NON TER 107 107 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64; Query Match 85.1%; Score 465.5; DB 4; Length 107; Best Local Similarity 85.8%; Pred. No. 3e-44; Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1; Qy 1 ELTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIYASNLQSGVPSRF 60 Db 3 QMTQSPSSLSASVGDRTVITCRASQISITVLNYYQKPGKAPKLLIYASNLQSGVPSRF 62 Qy 61 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTFGSGTKLEIKR 106 Db 63 SGSGSGTEFTLTISNLFQEDFASVYCOQSYTTLTFGSGTKLEIKR 107 RESULT 3 Q9UL81 PRELIMINARY; PRT; 107 AA. ID Q9UL81 AC Q9UL81; DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE Myosin-reactive immunoglobulin light chain variable region (Fragment). OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. OX NCBI\_TaxID=9606; FN [1] SEQUENCE FROM N.A. RP MEDLINE=98277139; PubMed=9614934; RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., RA Young D.C.;



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Best Local Similarity 78.1%; Pred. No. 4.5e-39;
Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRQSGISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 MTQSPSFSASVGDRTVITTCRASQISGLYAWYQKPGKAPQLIYAASLTQSGVPSRFS 83
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 GSGSGTFTLTISNLQFEDFASYCQSQSYTYTLTYFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 GSASGDTLTSLSCLOSEDFATYCCQYTYTPWTFGGTKVEIKR 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 75.5%; Score 413; DB 4; Length 108;
Best Local Similarity 77.1%; Pred. No. 2.2e-38;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRQSGISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 MTQSPSLSASVGDRTVITTCRMSQGISYLAWYQKPGKAPQLIYAASLTQSGVPSRFS 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 GSGSGTFTLTISNLQFEDFASYCQSQSYTYTLTYFGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 GSGSGTFTLTISNLQFEDFASYCQSQSYTYTLTYFGSGTKVEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC005332; AAH05332.1; -.

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[illegible]

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Db 3 QMTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 62
QY 61 SGSGSGTEFTLTISNLFQEDFASYQQSYTTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGGSATNFVTISSLQFEDFATYCCQYHLLPFTFGTKVDFKR 108

RESULT 11
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 68.4%; Score 374; DB 11; Length 234;
Best Local Similarity 69.8%; Pred. No. 1.3e-33;
Matches 74; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 QMTQSSLSASVGDRTVITCRARQISITVLYNWYQKPGDGVTKLLIYTTSSLHSGVPSRF 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGSGTEFTLTISNLFQEDFASYQQSYTTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 SGSGSGTHSLTISNLFQEDFATYCCQYHLLPFTFGTKLEIKR 128

RESULT 12
Q920E6 PRELIMINARY; PRT; 109 AA.
AC Q920E6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -.
DR PIR; S19112; S19112.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;

Query Match 68.2%; Score 373; DB 11; Length 109;
Best Local Similarity 66.0%; Pred. No. 6.6e-34;
Matches 70; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPASLSASVGEVTITCRASGNIHNLVLAQYQKSPQLLYVNATLADGVPSRF 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGSGTEFTLTISNLFQEDFASYQQSYTTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTQVSLKINSLQPEDFGSYQCQHFWSWTFGGTKLEIKR 108

RESULT 13
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; LWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 67.8%; Score 371; DB 4; Length 108;
Best Local Similarity 65.7%; Pred. No. 1.1e-33;
Matches 69; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRARQISITVLYNWYQKPGKAPKLLIWSASNLQSGVPSRF 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 MTQSFATLSVSPGERATLSCASQSVSSNLAWYQKPGQAPRELLYCASTRATGIPARF 63
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GSGSGTEFTLTISNLFQEDFASYQQSYTTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 GSGSGTEFTLTISNLFQEDFASYQCQHYNNWPFTEGPGTKVDIR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)";
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR PDB; 1CIC; 11-MAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K6Q; 18-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
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Query Match 67.3%; Score 368; DB 11; Length 214;
Best Local Similarity 65.1%; Pred. No. 5.6e-33;
Matches 69; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
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```
QY 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 QLTQSPASLSASVGEIVITCRASENIYSYLVANYQQKQKSPQLLYVNAKTLDAGVPSRF 82
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SSGSGGTFTLTISNLQFEDFASYCQSQSYTTLTYTFSGTKLEIKR 106
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 SGRSGTQFSLKINSIQPEDFGSYCQHHSGIPFTFGSGTKLEIKR 128
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: August 8, 2004, 12:17:46  
Job time : 29.0697 secs

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RESULT 15
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR PIR; B47329; B47329.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein_
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 67.1%; Score 367; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 8.1e-33;
```



PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 40; 45pp; English.

CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 60 light chain protein of the invention

XX Sequence 106 AA;

Query Match 98.2%; Score 537; DB 5; Length 106;  
 Best Local Similarity 99.1%; Pred. No. 4.4e-30;  
 Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRAQSISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 1 ELTQSPSLASVGDRTVITICRAQSISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60  
 QY 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 2

AAR54260  
 ID AAR54260 standard; protein; 107 AA.

XX AAR54260;

XX 25-MAR-2003 (revised)

DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b22.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
 KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
 KW framework; complementarity determining region.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21 /label= FR1

FT Region 22..33 /label= CDR1

FT Region 34..48 /label= FR2

FT Region 49..55 /label= CDR2

FT Region 56..87 /label= FR3

FT Region 88..95 /label= CDR3

FT Region 96..107 /label= FR4

XX WO9407922-A1.

PD 14-APR-1994.

XX 30-SEP-1993; 93WO-US0009328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI ) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or  
 PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro  
 PT diagnosis and for passive immuno-therapy.

XX Claim 5; Page 189; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification  
 CC using primers specific for heavy and light chain variable regions. The  
 CC amplification products were inserted into a dicistronic vector to produce  
 CC a library of fragments. E.coli XL1 Blue cells were transformed with the  
 CC library. Filamentous phage were produced which expressed the MAb regions  
 CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
 CC immunoreactive clones. The light chain VK region sequence AAR54260  
 CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 107 AA;

Query Match 88.5%; Score 484; DB 2; Length 107;

Best Local Similarity 88.7%; Pred. No. 2e-26;

Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITICRAQSISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 1 ELTQSPSLASVGDRTVITICRAQSISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

DB 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 3

AAR01283  
 ID AAR01283 standard; protein; 107 AA.

XX AAR01283;

XX 29-JAN-1997 (first entry)

XX VL region of HIV neutralising MAb, clone b22 and B35.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;  
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
 KW virus infectivity assay; precursor gp160; immunocompetence; human;  
 KW anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21 /label= FR1

FT Region 22..32 /label= CDR1

FT Region 33..47 /label= FR2

FT Region 48..54 /label= CDR2

FT Region 55..86 /label= FR3

FT Region 87..95 /label= CDR3

FT Region 96..107

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FT XX /label= FR4
PN XX WO9602273-A1.
PD XX 01-FEB-1996.
XX PF 11-JUL-1995; 95WO-US008743.
XX PR 18-JUL-1994; 94US-00276852.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1996-179601/18.
XX PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
PT immuno:therapy and detection of HIV infection.
XX PS Example; Fig 11; 366pp; English.
XX CC The sequences given in AA01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2 gene
CC clones, b22 and B35. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by
CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds
CC mature gp120 preferentially over the precursor gp160. The Mab may be used
CC for determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
XX SQ Sequence 107 AA;

Query Match 88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVLNWKQKPGKAPKLLIYAAASLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISISYLNWKQKPGKAPKLLIYAAASLQSGVPSRF 60
QY 61 SGSGSGTFTLTISNLFQEDFASYCQSYTTLTYFGSGTKLEIKR 106
Db 61 SGSGSGTFTLTISLQPEDFATYYCQSYSTPTTFGGTKLEIKR 106

RESULT 4
AA98244
ID AAY98244 standard; protein; 107 AA.
XX AC AAY98244;
XX DT 04-JUL-2000 (first entry)
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX OS Homo sapiens.
XX EN AU9948754-A.
XX PD 17-FEB-2000.
XX PF 16-SEP-1999; 99AU-00048754.
XX PR 16-SEP-1999; 99AU-00048754.
XX PA (SCRI ) SCRIPPS RES INST.

```

```

XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 2000-246867/22.
XX PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX PT (HIV) used for providing passive immunotherapy to HIV are specific for
XX PT Glycoprotein-120.
XX PS Example 9; Fig 11; 374pp; English.
XX CC This sequence represents a fragment of the antibodies of the invention.
XX CC The invention relates to the production of an anti-HIV (human
XX CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX CC of reducing an HIV infectivity titre in an in vitro virus infectivity
XX CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX CC production of the antibody comprises: (a) providing a first
XX CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX CC (which does not comprise the sequence represented by AA98206) and a
XX CC second polynucleotide encoding a light chain immunoglobulin amino acid
XX CC sequence; (b) inserting the first and second polynucleotide sequences
XX CC into a host cell; (c) maintaining the host cell in conditions which allow
XX CC the amino acid sequences encoded by the polynucleotides to be expressed
XX CC in the host cell; and (d) isolating the antibody comprising the heavy and
XX CC light chain immunoglobulin amino acid sequences from the host cell. The
XX CC anti-HIV gp-120 monoclonal antibody is used for providing passive
XX CC immunotherapy to HIV in a human. They can be administered to high-risk
XX CC patients to reduce the likelihood and/or severity of HIV-induced disease
XX CC and to patients who are already HIV-infected. The antibodies are used for
XX CC neutralising field isolates which provides information about the
XX CC immunocompetence of an immune response in HIV patients, for detecting HIV
XX CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX CC producing anti-idiotypic antibodies which can be used for active
XX CC immunisation and to screen human monoclonal antibodies to identify those
XX CC with the same binding specificity and to monitor the course of HIV
XX CC disease therapy by measuring the changes in concentration of HIV present
XX CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX CC monoclonal antibodies are encoded by a human polynucleotide sequence and
XX CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX CC reduce the problems of significant host immune response to the antibodies
XX CC associated with monoclonal antibodies of xenogeneic or chimeric
XX CC derivation
XX SQ Sequence 107 AA;

Query Match 88.5%; Score 484; DB 3; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVLNWKQKPGKAPKLLIYAAASLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISISYLNWKQKPGKAPKLLIYAAASLQSGVPSRF 60
QY 61 SGSGSGTFTLTISNLFQEDFASYCQSYTTLTYFGSGTKLEIKR 106
Db 61 SGSGSGTFTLTISLQPEDFATYYCQSYSTPTTFGGTKLEIKR 106

RESULT 5
AA95135
ID AAY95135 standard; protein; 107 AA.
XX AC AAY95135;
XX DT 30-JUN-2000 (first entry)
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX OS Homo sapiens.

```

XX AU9948756-A.  
 PN 17-FEB-2000.  
 PD 16-SEP-1999; 99AU-00048756.  
 PF 16-SEP-1999; 99AU-00048756.  
 PR (SCRI ) SCRIPPS RES INST.  
 PA Burton DR, Barbas CF, Lerner RA;  
 XX WFI; 2000-293393/26.  
 XX Novel human monoclonal antibodies which immunoreact with and neutralize  
 XX human immunodeficiency virus useful for treating HIV infections.  
 PT Example 9; Fig 11; 366pp; English.  
 PS  
 XX The present sequence represents a fragment of an anti-human  
 XX immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
 XX a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
 XX mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
 XX gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
 XX in vitro virus infectivity assay by 50% at a concentration of less than  
 XX 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
 XX immunotherapy of HIV induced disease. They are useful as neutralising  
 XX field isolates and provide useful information regarding the  
 XX immunocompetence of an immune response in HIV infected patients. The  
 XX monoclonal antibodies are useful for producing anti-idiotypic antibodies  
 XX which can be used to screen human monoclonal antibodies to identify  
 XX whether the antibody has the same binding specificity as the antibodies  
 XX of the invention. The neutralising antibodies define new epitopes on the  
 XX HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
 XX immunotherapeutic human monoclonal antibodies. A major advantage of the  
 XX monoclonal antibodies derives from the fact that they are encoded by a  
 XX human polynucleotide sequence. Thus in vivo use of the monoclonal  
 XX antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
 XX reduces the problems of significant host immune response to the passively  
 XX administered antibodies which is a problem commonly encountered when  
 XX monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
 XX An additional major advantage of the monoclonal antibodies described  
 XX derives from the fact that they immunoreact with a unique determinant  
 XX present on mature HIV glycoprotein gp120. This class of antibodies is  
 XX particularly effective at neutralising field isolates of HIV  
 XX  
 SQ Sequence 107 AA;  
 Query Match 88.5%; Score 484; DB 3; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 2e-26; Indels 0; Gaps 0;  
 Matches 94; Conservative 8; Mismatches 4;  
 QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
 QY 61 SGSGSGTEFTLTISLNQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
 DB 61 SGSGSGTDFTLTISLQPEDFATYCCQOSYSTPTPTFGQGTKEIKR 106  
 RESULT 6  
 AAG93590  
 ID AAG93590 standard; protein; 107 AA.  
 XX AAG93590;  
 AC AAG93590;  
 XX 14-SEP-2001 (first entry)  
 DT Human anti-Rh(D) chain I02 protein sequence.  
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
 XX Homo sapiens.  
 OS US6255455-B1.  
 PN 03-JUL-2001.  
 XX 29-JAN-1999; 99US-00240274.  
 PF 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA Siegel DL;  
 XX WFI; 2001-388931/41.  
 DR N-PSDB; AAH68647.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 XX diagnostics requiring a human instead of an animal antibody and in  
 XX therapeutic medicine.  
 PS Claim 1; Col 43; 162pp; English.  
 XX The present invention describes an isolated Rh(D) binding protein,  
 XX preferably a human antibody, (I) having an amino acid sequence comprising  
 XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 XX immunostimulant activity, and can be used as an immune system stimulant.  
 XX (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 XX are used in diagnostics that require human antibodies instead of animal  
 XX antibodies, such as determine the Rh phenotype of human red blood cells.  
 XX AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 XX chain CDR3 amino acid sequences which are given in the exemplification of  
 XX the present invention  
 XX  
 SQ Sequence 107 AA;  
 Query Match 88.3%; Score 483; DB 4; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 2.3e-26; Indels 0; Gaps 0;  
 Matches 93; Conservative 10; Mismatches 3;  
 QY 1 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVITTCRAQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61  
 QY 61 SGSGSGTEFTLTISLNQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
 DB 62 SGSGSGTDFTLTISLQPEDFATYCCQOSYSTPTPTFGQGTKEIKR 107  
 RESULT 7  
 ABO27397  
 ID ABO27397 standard; protein; 107 AA.  
 XX ABO27397;  
 AC ABO27397;  
 XX 12-SEP-2003 (first entry)  
 DT Anti-Rh(D) chain I02.  
 DE Human; RH(D) binding protein; blood typing; blood product; antibody;  
 XX magnetically activated cell sorting.  
 KW Homo sapiens.  
 OS US2003040605-A1.  
 XX 27-FEB-2003.  
 PD 27-FEB-2003.  
 XX



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PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0084045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR N-PSDB; ACD45311.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 4; Page 26; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;
XX
Query Match 88.3%; Score 483; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.3e-26;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVRTITCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLFQDFASVYCOQSYTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFTLTSSQLQDFATYCOQSYTLWTFGQTKVEIKR 107
RESULT 8
AAG93644
ID AAG93644 standard; protein; 107 AA.
XX
AC AAG93644;
XX
DT 14-SRP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH13 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0084045.
PR 10-APR-1998; 98US-0081380P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAG68701.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in

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PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Claim 1; Col 68; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC amino CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;
XX
Query Match 87.8%; Score 480; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.8e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVRTITCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDVRTITCRASQSISSYLNWYQKPGKAPKLLIYAASLSRSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLFQDFASVYCOQSYTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFTLTSSQLQDFATYCOQSYTLYTFGSGTKLEIKR 107
RESULT 9
ABO27451
ID ABO27451 standard; protein; 107 AA.
XX
AC ABO27451;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH13.
XX
KW Human; Rh(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0084045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR N-PSDB; ACD45365.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 4; Page 50; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC useful in various diagnostic and therapeutic applications in humans,

```

CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain  
XX  
SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 3.8e-26;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 61

QY 61 SGSGSGTEFTLTISNLFQFDPASYCQSYTTLTFCGSKLEIKR 106  
DB 62 SGSGSGTDFLTITISSLPQFDPATYCCQSYSTPTFTGGTKLEIKR 107

RESULT 10  
ID AAR54261 standard; protein; 107 AA.  
XX  
AC AAR54261;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)  
XX  
DE Anti-HIV gp120 immunoglobulin light chain variable region b27.  
XX  
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FR1  
FT Region 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT Region 49..55  
FT /label= CDR2  
FT Region 56..87  
FT /label= FR3  
FT Region 88..95  
FT /label= CDR3  
FT Region 96..107  
FT /label= FR4

XX WO9407922-A1.  
XX  
XX 14-APR-1994.  
XX  
XX 30-SEP-1993; 93WO-US009328.  
XX  
XX 30-SEP-1992; 92US-00954148.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Burton DR, Barbas CF, Lerner RA;  
XX  
XX WPI; 1994-135516/16.  
XX  
XX New human monoclonal antibodies neutralising HIV - react with gp120 or  
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro  
XX diagnosis and for passive immuno-therapy.  
XX  
XX Claim 5; Page 190; 248pp; English.  
XX  
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification  
XX using primers specific for heavy and light chain variable regions. The

CC amplification products were inserted into a dicistronic vector to produce  
CC a library of fragments. E.coli XL1 Blue cells were transformed with the  
CC library. Filamentous phage were produced which expressed the MAb regions  
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of  
CC immunoreactive clones. The light chain VK region sequence AAR54261  
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)  
XX  
SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 7.1e-26;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLFQFDPASYCQSYTTLTFCGSKLEIKR 106  
DB 61 SGSGSGTDFLTITISSLPQFDPATYCCQSYSTPTFTGGTKLEIKR 106

RESULT 11  
ID AAW01284 standard; protein; 107 AA.  
XX  
AC AAW01284;  
XX  
DT 29-JAN-1997 (first entry)  
XX  
DE VL region of HIV neutralising MAb, clone b27.  
XX  
KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;  
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
KW virus infectivity assay; precursor gp160; immunocompetence; human;  
KW anti-HIV antibody; detection; HIV infection.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FR1  
FT Region 22..32  
FT /label= CDR1  
FT Region 33..47  
FT /label= FR2  
FT Region 48..54  
FT /label= CDR2  
FT Region 55..86  
FT /label= FR3  
FT Region 87..95  
FT /label= CDR3  
FT Region 96..107  
FT /label= FR4

XX WO9602273-A1.  
XX  
XX 01-FEB-1996.  
XX  
XX 11-JUL-1995; 95WO-US008743.  
XX  
XX 18-JUL-1994; 94US-00276852.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Burton DR, Barbas CF, Lerner RA;  
XX  
XX WPI; 1996-179601/18.  
XX  
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive  
XX immuno:therapy and detection of HIV infection.  
XX  
XX Example; Fig 11; 366pp; English.  
XX  
XX



CC The present sequence represents a fragment of an anti-human  
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
CC in vitro virus infectivity assay by 50%, at a concentration of less than  
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
CC immunotherapy of HIV induced disease. They are useful as neutralising  
CC field isolates and provide useful information regarding the  
CC immunocompetence of an immune response in HIV infected patients. The  
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
CC which can be used to screen human monoclonal antibodies to identify  
CC whether the antibody has the same binding specificity as the antibodies  
CC of the invention. The neutralising antibodies define new epitopes on the  
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
CC immunotherapeutic human monoclonal antibodies. A major advantage of the  
CC monoclonal antibodies derives from the fact that they are encoded by a  
CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
CC reduces the problems of significant host immune response to the passively  
CC administered antibodies which is a problem commonly encountered when  
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
CC An additional major advantage of the monoclonal antibodies described  
CC derives from the fact that they immunoreact with a unique determinant  
CC present on mature HIV glycoprotein gp120. This class of antibodies is  
CC particularly effective at neutralising field isolates of HIV  
XX SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 7, 1e-26;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIYAASLSLQSGVPSRF 60  
Qy 61 SGSGSGTFTLTISNLQFEDFPASYCQSYTYLTTFGSGTKLEIKR 106  
Db 61 SGSGSGTFTLTISNLQFEDFPATYCCQSYSTPTQTFGGTKLEIKR 106

RESULT 14  
AAG93663  
ID AAG93663 standard; protein; 107 AA.  
AC AAG93663;  
XX 14-SEP-2001 (first entry)  
DE Human anti-Rh(D) antibody clone SH49 protein sequence.  
XX Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX Homo sapiens.  
OS US6255455-B1.  
XX 03-JUL-2001.  
XX 29-JAN-1999; 99US-00240274.  
XX 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-00884045.  
PR 10-APR-1998; 98US-0081380P.  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX Siegel DL;  
XX WPI; 2001-388931/41.  
DR N-PSDB; AAH68720.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX Claim 1; Col 69; 162pp; English.  
XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;  
Best Local Similarity 85.8%; Pred. No. 8, 3e-26;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
Db 2 ELTQSPSSLSASVGDRTVTTCRAQSIYSTYLNWYQKPGKAPKLLIYAASLSLQSGVPSRF 61  
Qy 61 SGSGSGTFTLTISNLQFEDFPASYCQSYTYLTTFGSGTKLEIKR 106  
Db 62 SGSGSGTFTLTISNLQFEDFPATYCCQSYSTPTQTFGGTKLEIKR 107

RESULT 15  
AAG93664  
ID AAG93664 standard; protein; 107 AA.

AC AAG93664;  
XX 14-SEP-2001 (first entry)  
DE Human anti-Rh(D) antibody clone SH50 protein sequence.  
XX Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.  
XX Homo sapiens.  
OS US6255455-B1.  
XX 03-JUL-2001.  
XX 29-JAN-1999; 99US-00240274.  
XX 11-OCT-1996; 96US-0028550P.  
PR 27-JUN-1997; 97US-00884045.  
PR 10-APR-1998; 98US-0081380P.  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX Siegel DL;  
XX WPI; 2001-388931/41.  
DR N-PSDB; AAH68720.  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX Claim 1; Col 69; 162pp; English.  
XX The present invention describes an isolated Rh(D) binding protein,  
CC

CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669, (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine, the antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAG68615 to AAG68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;  
Best Local Similarity 85.8%; Pred. No. 8.3e-26;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ELTQSPSSLSASVGRVTITCRQSIQSYLNWYQKPKAPKLLIWAASNLQSGVPSRF 60  
Db 2 ELTQSPSSLSASVGRVTITCRQSIQSYLNWYQKPKAPKLLIWAASNLQSGVPSRF 61  
Qy 61 SGSGSGTEFTLTIINLQFEDFASYCQOSYTLVTFGSGTKLEIKR 106  
Db 62 SGSGSGTDFTLTISSLPQEDFATYCCQSYSTPWFQSGIKVEIKR 107

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OM protein - protein search, using sw model

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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	100.0	106	14	US-10-027-725A-11
2	484	88.5	107	14	US-10-016-986-104
3	483	88.3	107	10	US-09-848-798-33
4	480	87.0	107	10	US-09-848-798-156
5	476	87.0	107	14	US-10-016-986-105
6	475	86.8	107	10	US-09-848-798-175
7	475	86.8	107	10	US-09-848-798-176
8	474	86.7	107	10	US-09-848-798-179
9	473.5	86.6	108	10	US-09-848-798-32
10	473.5	86.6	108	10	US-09-848-798-43
11	473	86.5	107	10	US-09-848-798-37
12	473	86.5	111	14	US-10-203-754A-57
13	472.5	86.4	108	10	US-09-848-798-167
14	472	86.3	107	10	US-09-848-798-38
15	472	86.3	107	10	US-09-848-798-39

16	472	86.3	107	10	US-09-848-798-162	Sequence 162, App
17	471	86.1	107	10	US-09-848-798-158	Sequence 158, App
18	469	85.7	107	10	US-09-848-798-44	Sequence 44, Appl
19	468	85.6	111	14	US-10-203-754A-56	Sequence 56, Appl
20	467	85.4	240	9	US-09-192-854-2	Sequence 2, Appli
21	467	85.4	240	9	US-09-968-561A-2	Sequence 2, Appli
22	467	85.4	240	10	US-09-968-744A-2	Sequence 2, Appli
23	467	85.4	240	12	US-09-968-561A-2	Sequence 2, Appli
24	466	85.2	107	10	US-09-791-153A-67	Sequence 67, Appl
25	465.5	85.1	107	12	US-10-460-595-9	Sequence 9, Appli
26	465	85.0	107	15	US-10-309-762-89	Sequence 89, Appl
27	464.5	84.9	108	10	US-09-848-798-163	Sequence 163, App
28	463	84.6	104	14	US-10-016-986-106	Sequence 106, App
29	463	84.6	107	15	US-10-309-762-88	Sequence 88, Appl
30	462	84.5	127	15	US-10-309-762-101	Sequence 101, App
31	460.5	84.2	107	12	US-10-363-349-4	Sequence 4, Appli
32	460.5	84.2	288	12	US-10-363-349-7	Sequence 7, Appli
33	460	84.1	106	14	US-10-027-725A-10	Sequence 10, Appl
34	459	83.9	107	10	US-09-848-798-168	Sequence 168, App
35	459	83.9	233	16	US-10-663-244-150	Sequence 150, App
36	458	83.7	106	15	US-10-377-121-5	Sequence 5, Appli
37	457	83.5	107	10	US-09-848-798-36	Sequence 36, Appl
38	457	83.5	214	14	US-10-153-382-19	Sequence 19, Appl
39	456.5	83.5	108	10	US-09-848-798-41	Sequence 41, Appl
40	456.5	83.5	108	14	US-10-016-986-109	Sequence 109, App
41	456	83.4	105	15	US-10-309-762-155	Sequence 155, App
42	456	83.4	107	10	US-09-848-798-173	Sequence 173, App
43	456	83.4	107	15	US-10-309-762-67	Sequence 67, Appl
44	456	83.4	107	15	US-10-309-762-68	Sequence 68, Appl
45	455	83.2	107	16	US-10-723-434-40	Sequence 40, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-027-725A-11  
; Sequence 11, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-11

Query Match	100.0%;	Score 547;	DB 14;	Length 106;
Best Local Similarity	100.0%;	Pred. No. 1.2e-41;		
Matches 106;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	ELTQSPSSLASVGDRTVITTCRROSISTYLNWYQKPKAPKLLIWSASNLQSGVPSRF	60	
Db	1	ELTQSPSSLASVGDRTVITTCRROSISTYLNWYQKPKAPKLLIWSASNLQSGVPSRF	60	
QY	61	SGSGSGTFTLTISNLQFEDFASYCQSYTLYTFGSGTKLEIKR	106	
Db	61	SGSGSGTFTLTISNLQFEDFASYCQSYTLYTFGSGTKLEIKR	106	

##### RESULT 2

US-10-016-986-104  
; Sequence 104, Application US/10016986  
; Publication No. US20030187247A1  
; GENERAL INFORMATION:

Db	2	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61
Qy	61	SGSGSGTFTLTISNLFQDFASVYCOOSYTLTFTGSGTKLEIKR	106
Db	62	SGSGSGTFTLTISNLFQDFATYCCQSYSTLWTFGGTKVEIKR	107
RESULT 4			
US-09-848-798-156			
; Sequence 156, Application US/09848798			
; Publication No. US20030040605A1			
; GENERAL INFORMATION:			
; APPLICANT: Siegel, Donald L.			
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL			
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF			
; FILE REFERENCE: 09596-42U2			
; CURRENT APPLICATION NUMBER: US/09/848,798			
; CURRENT FILING DATE: 2001-05-04			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274			
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550			
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11			
; NUMBER OF SEQ ID NOS: 224			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 156			
; LENGTH: 107			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13			
US-09-848-798-156			
Query Match 87.8%; Score 480; DB 10; Length 107;			
Best Local Similarity 87.7%; Pred. No. 1.2e-35;			
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;			
Qy	1	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60
Db	2	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61
Qy	61	SGSGSGTFTLTISNLFQDFASVYCOOSYTLTFTGSGTKLEIKR	106
Db	62	SGSGSGTFTLTISNLFQDFATYCCQSYSTLWTFGGTKLEIKR	107
RESULT 5			
US-10-016-986-105			
; Sequence 105, Application US/10016986			
; Publication No. US20030187247A1			
; GENERAL INFORMATION:			
; APPLICANT: Burton, Dennis R			
; APPLICANT: Barbas, Carlos F			
; APPLICANT: Lerner, Richard A			
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES			
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS			
; FILE REFERENCE: 313.2CON1			
; CURRENT APPLICATION NUMBER: US/10/016,986			
; CURRENT FILING DATE: 2001-12-12			
; PRIOR APPLICATION NUMBER: US 09/149,898			
; PRIOR FILING DATE: 1998-09-08			
; PRIOR APPLICATION NUMBER: US 08/899,575			
; PRIOR FILING DATE: 1997-07-24			
; PRIOR APPLICATION NUMBER: US 08/276,852			
; PRIOR FILING DATE: 1994-07-18			
; PRIOR APPLICATION NUMBER: US 08/178,302			
; PRIOR FILING DATE: 1994-01-06			
; PRIOR APPLICATION NUMBER: PCT/US93/09328			
; PRIOR FILING DATE: 1993-09-30			
; PRIOR APPLICATION NUMBER: US 07/954,148			
; PRIOR FILING DATE: 1992-09-30			
; NUMBER OF SEQ ID NOS: 176			
; SOFTWARE: FastSeq for Windows Version 4.0			

Db	2	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61
Qy	61	SGSGSGTFTLTISNLFQDFASVYCOOSYTLTFTGSGTKLEIKR	106
Db	62	SGSGSGTFTLTISNLFQDFATYCCQSYSTLWTFGGTKVEIKR	107
RESULT 4			
US-09-848-798-156			
; Sequence 156, Application US/09848798			
; Publication No. US20030040605A1			
; GENERAL INFORMATION:			
; APPLICANT: Siegel, Donald L.			
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL			
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF			
; FILE REFERENCE: 09596-42U2			
; CURRENT APPLICATION NUMBER: US/09/848,798			
; CURRENT FILING DATE: 2001-05-04			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274			
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550			
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11			
; NUMBER OF SEQ ID NOS: 224			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 156			
; LENGTH: 107			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13			
US-09-848-798-156			
Query Match 87.8%; Score 480; DB 10; Length 107;			
Best Local Similarity 87.7%; Pred. No. 1.2e-35;			
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;			
Qy	1	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60
Db	2	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61
Qy	61	SGSGSGTFTLTISNLFQDFASVYCOOSYTLTFTGSGTKLEIKR	106
Db	62	SGSGSGTFTLTISNLFQDFATYCCQSYSTLWTFGGTKLEIKR	107
RESULT 5			
US-10-016-986-105			
; Sequence 105, Application US/10016986			
; Publication No. US20030187247A1			
; GENERAL INFORMATION:			
; APPLICANT: Burton, Dennis R			
; APPLICANT: Barbas, Carlos F			
; APPLICANT: Lerner, Richard A			
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES			
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS			
; FILE REFERENCE: 313.2CON1			
; CURRENT APPLICATION NUMBER: US/10/016,986			
; CURRENT FILING DATE: 2001-12-12			
; PRIOR APPLICATION NUMBER: US 09/149,898			
; PRIOR FILING DATE: 1998-09-08			
; PRIOR APPLICATION NUMBER: US 08/899,575			
; PRIOR FILING DATE: 1997-07-24			
; PRIOR APPLICATION NUMBER: US 08/276,852			
; PRIOR FILING DATE: 1994-07-18			
; PRIOR APPLICATION NUMBER: US 08/178,302			
; PRIOR FILING DATE: 1994-01-06			
; PRIOR APPLICATION NUMBER: PCT/US93/09328			
; PRIOR FILING DATE: 1993-09-30			
; PRIOR APPLICATION NUMBER: US 07/954,148			
; PRIOR FILING DATE: 1992-09-30			
; NUMBER OF SEQ ID NOS: 176			
; SOFTWARE: FastSeq for Windows Version 4.0			

Db	2	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61
Qy	61	SGSGSGTFTLTISNLFQDFASVYCOOSYTLTFTGSGTKLEIKR	106
Db	62	SGSGSGTFTLTISNLFQDFATYCCQSYSTLWTFGGTKVEIKR	107
RESULT 4			
US-09-848-798-156			
; Sequence 156, Application US/09848798			
; Publication No. US20030040605A1			
; GENERAL INFORMATION:			
; APPLICANT: Siegel, Donald L.			
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL			
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF			
; FILE REFERENCE: 09596-42U2			
; CURRENT APPLICATION NUMBER: US/09/848,798			
; CURRENT FILING DATE: 2001-05-04			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274			
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550			
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11			
; NUMBER OF SEQ ID NOS: 224			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 156			
; LENGTH: 107			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: anti-Rh(D) chain I02			
US-09-848-798-33			
Query Match 88.3%; Score 483; DB 10; Length 107;			
Best Local Similarity 87.7%; Pred. No. 6.6e-36;			
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;			
Qy	1	ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60



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; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match
Best Local Similarity 87.0%; Score 476; DB 14; Length 107;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIYAASLQSGVPSRF 60
Qy 61 SSGSGTEFTLTISNLQFDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 61 SSGSGTDFLTITSSLPQDFATYCCQSYSTPTQTFGGTKVEIKR 106

RESULT 6
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match
Best Local Similarity 86.8%; Score 475; DB 10; Length 107;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIYAASLQSGVPSRF 61
Qy 61 SSGSGTEFTLTISNLQFDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQDFATYCCQSYSTPTQTFGGTKVEIKR 107

RESULT 7
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match
Best Local Similarity 86.7%; Score 474; DB 10; Length 107;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIYAASLQSGVPSRF 61
Qy 61 SSGSGTEFTLTISNLQFDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQDFATYCCQSYSTPTQTFGGTKVEIKR 107

RESULT 9
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match
Best Local Similarity 85.8%; Score 474; DB 10; Length 107;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQISITVLNWKQKPGKAPKLLIYAASLQSGVPSRF 61
Qy 61 SSGSGTEFTLTISNLQFDFASYCQOSYTYLTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQDFATYCCQSYSTPTQTFGGTKVEIKR 107

RESULT 9
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.8e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITTCRARSISSTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61

QY 61 SGSGSGTEFTLTISNLQPEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPQEDFATYCCQSYSTPTPTFGQTKLEIKR 108

RESULT 10
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.8e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITTCRARSISSTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61

QY 61 SGSGSGTEFTLTISNLQPEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPQEDFATYCCQSYSTPTPTFGQTKLEIKR 108

RESULT 11
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      86.5%; Score 473; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.2e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITTCRARSISSTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61

QY 61 SGSGSGTEFTLTISNLQPEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPQEDFATYCCQSYSTPTPTFGQTKLEIKR 107

RESULT 12
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-754A-57

Query Match      86.5%; Score 473; DB 14; Length 111;
Best Local Similarity 86.7%; Pred. No. 5.4e-35;
Matches 91; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61
Db 4 MTQSPSSLASVGDRTVITTCRARSISSTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 63

QY 62 SGSGSGTEFTLTISNLQPEDFASYCQSQSYTT-LYTFGSGTKLEIKR 106
Db 64 SGSGSGTDFLTITSSLPQEDFATYCCQSYTPTPTFGQTKLEIKR 108

RESULT 13
US-09-848-798-167
; Sequence 167, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 167
; LENGTH: 108
; TYPE: ERT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-848-798-167

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Query Match	86.4%	Score 472.5	DB 10	Length 108
Best Local Similarity	87.9%	Pred. No. 5.9e-35		
Matches	94	Conservative	7	Mismatches 5
			Indels	1
			Gaps	1
QY	1	ELTQSPSSLASVGDRTVITTCRAQSTISTYLNWYQQKPGKAPKLLIWSAGNLSQGVSRF	60	
Db	2	ELTQSPSSLASVGDRTVITTCRASQSTISSYLNWYQQKPGKAPKLLIYASGLSQGVSRF	61	
QY	61	SGSGSGTEFTLITSLNQLQDFASFYCCQSYTT-LYTFSGTGKLEIKR	106	
Db	62	SGSGSGTDFLTLSLQDFATFYCCQSYSTPPYTFGGTGKLEIKR	108	

RESULT 14

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US-09-848-798-38
; Sequence 38, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 03596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-848-798-38

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Query Match      86.3%; Score 472; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 6.4e-35;
Matches          92; Conservative    9; Mismatches   5; Indels     0; Gaps     0;

QY      1 ELTQSPSSISASVGDRTVITCRARQSISIVLNYYQQKPGKAPKLLIWSANLSQGVSRRF 60
         |||||.....:|||.....:|||||.....:|||||.....:|||||.....:
Db       2 ELTQSPSSI SASVGDRTVITCRASQSISSVLNYYQQKPGKAPKLLIIAASSLQSGVPSNF 61
         |||||.....:|||.....:|||||.....:|||||.....:|||||.....:

QY      61 SGGSGCTETLTISNLQDFEFASYCQOSYTTLTYFGSGTKLEIKR 106
         |||||.....:|||.....:|||||.....:|||||.....:|||||.....:
Db       62 SGGSGGDTFLTATSSLQDDEFATNYCQOSYSTRPTFGGGTKVEIKR 107
         |||||.....:|||.....:|||||.....:|||||.....:|||||.....:
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## RESULT 15

US-09-848-798-39

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; Sequence 39, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I08
US-09-848-798-39

Query Match      86.3%; Score 472; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 6,4e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0

QY      1 ELTQPSLSASVGRVITTCRAQSISTYLNWYQQKPGKAPKLLIWSASLQSGVPSRF 60
Db      2 ELTQPSLSASVGRVITTCRAQSISTYLNWYQQKPGKAPKLLIYAASLQSGVPSRF 61
QY      61 SGSGSGTFTLTLSLQPEDFASYVCQSYTTLTFTSGGKLEIKR 106
Db      62 SGSGSGTFTLTLSLQPEDFATYVCQSYTPTFTGGTKVEIKR 107

Search completed: August 8, 2004, 12:43:21
Job time : 35.8152 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 12.6879 Seconds  
(without alignments)  
431.306 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSSLASVGDRTVIT.....QQSYTYLYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	88.5	107	1	US-08-276-852-104
2	484	88.5	107	1	US-08-899-575-104
3	484	88.5	107	1	US-08-899-575-104
4	484	88.5	107	5	PCT-US95-08743-104
5	483	88.3	107	3	US-09-240-274-33
6	480	87.8	107	3	US-09-240-274-156
7	476	87.0	107	1	US-08-276-852-105
8	476	87.0	107	1	US-08-899-575-105
9	476	87.0	107	1	US-08-899-575-105
10	476	87.0	107	5	PCT-US95-08743-105
11	475	86.8	107	3	US-09-240-274-175
12	475	86.8	107	3	US-09-240-274-176
13	474	86.7	107	3	US-09-240-274-179
14	473.5	86.6	108	3	US-09-240-274-32
15	473.5	86.6	108	3	US-09-240-274-43
16	473	86.5	107	3	US-09-240-274-37
17	472.5	86.4	108	3	US-09-240-274-167
18	472	86.3	107	3	US-09-240-274-38
19	472	86.3	107	3	US-09-240-274-39
20	472	86.3	107	3	US-09-240-274-162
21	471	86.1	107	3	US-09-240-274-158
22	469	85.7	107	3	US-09-240-274-44
23	468	85.6	108	2	US-08-379-057-29
24	464.5	84.9	108	3	US-09-240-274-163
25	463	84.6	104	1	US-08-276-852-106
26	463	84.6	104	1	US-08-899-575-106
27	463	84.6	104	1	US-08-899-575-106

#### ALIGNMENTS

RESULT 1  
US-08-276-852-104  
; Sequence 104, Application US/08276852  
; Patent No. 5652138  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; NUMBER OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/276,852  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCL1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-276-852-104

Sequence 106, App  
Sequence 14, Appl  
Sequence 66, Appl  
Sequence 66, Appl  
Sequence 168, App  
Sequence 66, Appl  
Sequence 36, Appl  
Sequence 3, Appl  
Sequence 71, Appl  
Sequence 109, App  
Sequence 109, App  
Sequence 109, App  
Sequence 41, Appl  
Sequence 109, App  
Sequence 173, App  
Sequence 103, App  
Sequence 103, App  
Sequence 103, App

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 1.4e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNWNQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNWNQKPGKAPKLLIWAASLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTTLTYFGSGTKLEIKR 106  
DB 61 SGSGSGTDFLTITSLQPEDFATYCCQSYSTPTFTFGQGTKEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 1.4e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNWNQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNWNQKPGKAPKLLIWAASLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTTLTYFGSGTKLEIKR 106  
DB 61 SGSGSGTDFLTITSLQPEDFATYCCQSYSTPTFTFGQGTKEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 1.4e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNWNQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITCRASQISITLYNWNQKPGKAPKLLIWAASLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTTLTYFGSGTKLEIKR 106  
DB 61 SGSGSGTDFLTITSLQPEDFATYCCQSYSTPTFTFGQGTKEIKR 106

RESULT 4  
PCT-US95-08743-104  
; Sequence 104, Application PC/TUS9508743

```

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BFO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      88.5%; Score 483; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-36;
Matches 94; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVLNYYQKPKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCRASQISITVLNYYQKPKAPKLLIWAASLQSGVPSRF 60
QY 61 SGGSGTFTLTISNLQFEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 61 SGGSGTFTLTISNLQFEDFATYCCQSYSTPYTFGGTKVEIKR 106

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-33

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.7e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVLNYYQKPKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISITVLNYYQKPKAPKLLIWAASLQSGVPSRF 61
QY 61 SGGSGTFTLTISNLQFEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 62 SGGSGTFTLTISNLQFEDFATYCCQSYSTPYTFGGTKVEIKR 107

RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.2e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVLNYYQKPKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISITVLNYYQKPKAPKLLIWAASLQSGVPSRF 61
QY 61 SGGSGTFTLTISNLQFEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 62 SGGSGTFTLTISNLQFEDFATYCCQSYSTPYTFGGTKVEIKR 107

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652136
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

```

RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.2e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQISITVLNYYQKPKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISITVLNYYQKPKAPKLLIWAASLQSGVPSRF 61
QY 61 SGGSGTFTLTISNLQFEDFASYCQOSYTYLTFTGSGTKLEIKR 106
Db 62 SGGSGTFTLTISNLQFEDFATYCCQSYSTPYTFGGTKVEIKR 107

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652136
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105

Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITCRARQSIGISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLASVGDRTVITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60

Qy 61 SGSGSGTEFTLTISNLOFEDFASYYCOOSYTLTYTSGTKLEIKR 106
Db 61 SGSGSGTDFLTITSSLPEDFATYYCOOSYSTPTQTGGTKLEIKR 106

RESULT 8
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105

; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105
```



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Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 60
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 106
Db 61 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 106

RESULT 10
PCT-US95-08743-105
; Sequence 105, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match      87.0%; Score 476; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.4e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 60
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 106
Db 61 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 106

RESULT 11
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 9.1e-36;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 106
Db 62 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 107

RESULT 12
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 9.1e-36;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCARQSIISTYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 106
Db 62 SSGSGTFTLTISNLQPEDFASYCQSYSTLTLYTFGSGTKLEIKR 107

RESULT 13
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      86.6%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.1e-35;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SSGSGTFTLTITSNLQFEDFASYCQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPWTFGGKVEIKR 107

RESULT 14
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32
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; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SSGSGTFTLTITSNLQFEDFASYCQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPWTFGGKVEIKR 108

Search completed: August 8, 2004, 12:20:25
Job time : 13.6879 secs
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Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SSGSGTFTLTITSNLQFEDFASYCQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPWTFGGKVEIKR 108

RESULT 15
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

```
Query Match      86.6%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.1e-35;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIYSTVYNWYQKPGKAPKLLIYAASLQSGVPSRF 61

Qy 61 SSGSGTFTLTITSNLQFEDFASYCQSYTT-LYTFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPQEDFATYCCQSYSTPWTFGGKVEIKR 107

RESULT 14
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 9.31515 Seconds  
(without alignments)  
1094.593 Million cell updates/sec

Title: US-10-027-725A-12  
Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPYTFGQGTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	84.2	117	2 S46376	Ig kappa chain V-J
2	462	84.2	125	2 S40316	Ig kappa chain - h
3	459	83.6	125	2 S40333	Ig kappa chain V-J
4	455	82.9	125	2 S40349	Ig kappa chain V-J
5	454.5	82.8	124	2 S40336	Ig kappa chain V-J
6	454	82.7	130	2 S40368	Ig kappa chain - h
7	451	82.1	128	2 S46372	Ig kappa chain var
8	451	82.1	131	2 S40352	Ig kappa chain V-J
9	450	82.0	105	2 S36266	Ig kappa chain V-J
10	447	81.4	127	2 S40367	Ig kappa chain V-J
11	446	81.2	108	2 S19674	Ig kappa chain V-J
12	446	81.2	132	2 S38646	Ig kappa chain V-J
13	445	81.1	117	2 S46371	Ig kappa chain V-J
14	444	80.9	123	2 S40331	Ig kappa chain - h
15	444	80.9	132	2 S40334	Ig kappa chain - h
16	443	80.7	108	2 B49047	Ig kappa chain V-J
17	441	80.3	108	2 S47182	Ig kappa chain - h
18	441	80.3	109	2 S31998	Ig kappa chain - h
19	441	80.3	124	2 S40318	Ig kappa chain V-J
20	439.5	80.1	108	2 S30521	Ig kappa chain V-J
21	439	80.0	109	2 S40369	Ig kappa chain V-J
22	437	79.6	107	2 S36264	Ig kappa chain V-J
23	435.5	79.3	108	2 S34007	Ig kappa chain V-J
24	435	79.2	108	1 K1HUBN	Ig kappa chain V-J
25	434.5	79.1	107	2 S36275	Ig kappa chain V-J
26	434	79.1	108	1 K1HUBS	Ig kappa chain V-J
27	434	79.1	108	2 S44122	Ig kappa chain V-J
28	433	78.9	117	2 S21527	Ig kappa chain pre
29	432	78.7	108	2 S36283	Ig kappa chain V-J

#### ALIGNMENTS

##### RESULT 1

S46376

Ig kappa chain V-J region (T33-14) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C:Accession: S46376; S38649

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re

A:Reference number: S46369; MUID:9431375; PMID:8039491

A:Accession: S46376

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:Z27177; NID:g415969; PIDN:CAA81701.1; PID:g415970

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:25-99/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 117;

Best Local Similarity 84.9%; Pred. No. 2e-32; Mismatches 0; Gaps 0;

Matches 90; Conservative 7; Indels 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHQPAPKLLIYASLSQSGVPSRF 60

Db ::|

12 QMTQSPSSVSASIGDRVTITCRASQDISWLAHYQOKPGKAPKLLIYAASSLQSGVPLRF 71

QY 61 SSGSGYGTDFSLTISLSI-OFEDSATYTCQANSFPYTFGQGTKVEIKR 106

Db ::|

72 SSGSGYGTDFSLTISLSI-OFEDSATYTCQANSFPYTFGQGTKVEIKR 117

##### RESULT 2

S40316

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40316

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40316

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72426

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 125;

Best Local Similarity 85.8%; Pred. No. 2.2e-32;

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Matches 91; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 18 QLTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYHISLQTVPSRF 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 SGSGSGTDFLTISLQPEDFATYCCQANSFPYTFGGTKVEIKR 123
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 459; DB 2; Length 125;
Best Local Similarity 82.9%; Pred. No. 3.9e-32;
Matches 87; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 QMTQSPSLASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYKASSLSQGVPSRF 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SGSGSGTEFTLTISLQPEDFATYCCQANSFPYTFGGTKVEIK 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40349
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 455; DB 2; Length 125;
Best Local Similarity 84.9%; Pred. No. 8.5e-32;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QLTQSPSLASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYDASSLSQGVPSRF 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 SGSGSGTDFLTISLQPEDFATYCCQANSFPYTFGGTKVEIKR 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 5
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40336
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-124 <KLE>
A:Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 454.5; DB 2; Length 124;
Best Local Similarity 84.1%; Pred. No. 9.3e-32;
Matches 90; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 18 QLTQSPSLASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYAASTLSQGVPSRF 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 SGSGSGTEFTLTISLQPEDFATYCCQANSFPYTFGGTKVEIKR 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
S40368
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40368
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40368
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-130 <KLE>
A:Cross-references: EMBL:X72478; NID:g441424; PIDN:CAA51146.1; PID:g441425
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 454; DB 2; Length 130;
Best Local Similarity 83.0%; Pred. No. 1.1e-31;
Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QMTQSPSSVSASVGDRTVITCRASQDVAGWLAHYQHOPGKAPKLLIYAASTLSQGVPSRF 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 SGSGSGTDFLTISLQPEDFATYCCQANSFPYTFGGTKVEIKR 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
S46372
IG light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46372
R:Benjamin, C.; Chastagner, P.; Zouali, M.
```

C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 450; DB 2; Length 105;  
Best Local Similarity 85.3%; Pred. No. 1.9e-31;  
Matches 87; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 LTQSPSSVASVGDRTVITCRASQGISWLAUWHQPGKAPKLLIYSASSLSQSGVPSRF 61  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
4 LTQSPSSVASVGDRTVITCRASQGISRWLAUWHQPGKAPNLLIYAASTLETGVPSPRS 63

QY 62 GSGYGTDFTLTISSLQPEDSATYYCOANSFPYTFGGTKVE 103  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
64 GSGSGTDFLTIISSLQPEDFATYYCOANSFPLTFGGGTKLE 105

RESULT 10  
S19674  
Ig kappa chain V-J-C region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40367  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40367  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A;Residues: 1-127 <KLE>  
A;Cross-references: EMBL:X72477  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 447; DB 2; Length 127;  
Best Local Similarity 82.1%; Pred. No. 4.1e-31;  
Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRVTITCRASQGISWLAUWHQPGKAPKLLIYSASSLSQSGVPSRF 60  
Db : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
20 QMTQSPSSLASVGDRVTITCRASQSISNYLNWYQRKPGRAPKLLIYAASLSQSGVPSRF 79

QY 61 SGSGYGTDFSLTISSLQPEDSATYYCOANSFPYTFGGTKVEIKR 106  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
80 SGSGSGTDFLTIISSLQPEDFATYYCOASYNTDWTFGGTKVEIKR 125

RESULT 11  
S19674  
Ig kappa chain V region (clone alpha-TEL9) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C;Accession: S19674  
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991  
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p  
A;Reference number: S19663; MUID:92085276; PMID:1748994  
A;Accession: S19674  
A:Molecule type: mRNA  
A;Residues: 1-108 <MAR>  
A;Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g133586  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 108;  
Best Local Similarity 82.9%; Pred. No. 4.2e-31;  
Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSVASVGDRTVITCRASQGISWLAUWHQPGKAPKLLIYSASSLSQSGVPSRF 61  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
4 LTQSPSSLASVGDRTVITCRASQGISNYLNWYQRKPGRAPKLLIYAASLTQSGVPSRF 63

[illegible]

Search completed: August 8, 2004, 12:18:55  
Job time : 9.31515 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 5.78182 Seconds  
(without alignments)  
954.620 Million cell updates/sec

Title: US-10-027-725A-12  
Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGRVTTIT.....QANSPFYTFGGTKVFIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	435	79.2	108	1	KV1V_HUMAN
2	434	79.1	108	1	KV1S_HUMAN
3	426.5	77.7	107	1	KV1D_HUMAN
4	424	77.2	108	1	KV1R_HUMAN
5	424	77.2	129	1	KV1W_HUMAN
6	423	77.0	108	1	KV1G_HUMAN
7	423	77.0	108	1	KV1H_HUMAN
8	419	76.3	108	1	KV1F_HUMAN
9	419	76.3	108	1	KV1L_HUMAN
10	416	75.8	108	1	KV1O_HUMAN
11	413	75.2	108	1	KV1B_HUMAN
12	410	74.7	108	1	KV1M_HUMAN
13	408	74.3	108	1	KV1E_HUMAN
14	406	74.0	108	1	KV1A_HUMAN
15	405	73.8	108	1	KV1P_HUMAN
16	402	73.2	117	1	KV1I_HUMAN
17	401	73.0	108	1	KV1N_HUMAN
18	401	73.0	108	1	KV1Y_HUMAN
19	394	71.8	117	1	KV1J_HUMAN
20	393	71.6	108	1	KV1K_HUMAN
21	391	71.2	108	1	KV1Q_HUMAN
22	385	70.1	108	1	KV1X_HUMAN
23	385	70.1	129	1	KV1S_MOUSE
24	383	69.8	108	1	KV5S_MOUSE
25	380	69.2	108	1	KV5T_MOUSE
26	376	68.5	108	1	KV5K_MOUSE
27	373	67.9	108	1	KV1T_HUMAN
28	370.5	67.5	109	1	KV5E_MOUSE
29	370	67.4	128	1	KV5L_MOUSE
30	368	67.0	108	1	KV5O_MOUSE
31	368	67.0	108	1	KV4C_HUMAN
32	368	67.0	134	1	KV3M_HUMAN
33	367.5	66.9	129	1	P18136 homo sapien

34	366.5	66.8	129	1	KV3L_HUMAN	P18135 homo sapien
35	366	66.7	108	1	KV5P_MOUSE	P01649 mus musculus
36	366	66.7	108	1	KV5R_MOUSE	P01651 mus musculus
37	366	66.7	114	1	KV4A_HUMAN	P01625 homo sapien
38	364.5	66.4	109	1	KV3D_HUMAN	P01622 homo sapien
39	363.5	66.2	109	1	KV3B_HUMAN	P01620 homo sapien
40	363	66.1	108	1	KV5M_MOUSE	P01646 mus musculus
41	362	65.9	111	1	KV3L_MOUSE	P01664 mus musculus
42	361.5	65.8	109	1	KV3F_HUMAN	P01624 homo sapien
43	361.5	65.8	129	1	KV3H_HUMAN	P04207 homo sapien
44	361	65.8	108	1	KV5N_MOUSE	P01647 mus musculus
45	359	65.4	111	1	KV3M_MOUSE	P01665 mus musculus

ALIGNMENTS

RESULT 1  
KV1V\_HUMAN  
ID KV1V\_HUMAN STANDARD; PRT; 108 AA.  
AC P04430;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-1 region BAN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=66174817; PubMed=3083240;  
RA Dwulet F.E., O'Connor T.P., Benson M.D.;  
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
RL Mol. Immunol. 23:73-78(1986).  
DR PIR; A01878; KIHUEN.  
DR HSSP; P80362; IWTLL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Amyloid.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 79.2%; Score 435; DB 1; Length 108;  
Best Local Similarity 78.3%; Pred No. 1.9e-38;  
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY	1	ELTQSPSSVSASVGRVTTITCRASGISLAWYQHFGKAPKLIYASISLQSGVPSRF	60
Db	3	QLTQSPSSLSASVGRVTTITCRASGVNYVAWFQKFKAPKSLIYDASTLQSGVPSNF	62
QY	61	SSGSGTDFSTLISLQFSDSATYTCQANSEPFYTFGGTKVFIKR	106
Db	63	TSGSGTDFILTISLQFEDFATYTCQYNSPYTFGGTKVQIKR	108

RESULT 2  
KV1S\_HUMAN  
ID KV1S\_HUMAN STANDARD; PRT; 108 AA.

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AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01877; KIHUWS.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B1A649A60E45 CRC64;

Query Match 79.1%; Score 434; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.4e-38;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQDISHLWAWYQKSGKAPKLLIYSASSLSQSGVPSRF 62
QY 61 SSGSGVGTDFSLTISSLPEDSATYCCQANSFPYTFGQGTKEIKR 106
DB 63 SSGSGGTFTLTISLSPEDFATYCCQAHSPVLTFGGTTVDIKR 108

Query Match 79.1%; Score 426.5; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 1.4e-37;
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQDISHLWAWYQKSGKAPKLLIYSASSLSQSGVPSRF 62
QY 61 SSGSGVGTDFSLTISSLPEDSATYCCQANSFPYTFGQGTKEIKR 106
DB 63 SSGSGGTFTLTISLSPEDFATYCCQYNTF-FTFGPTKVDIKR 107

RESULT 3
KVLD HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein.";
```

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RL Eur. J. Biochem. 49:377-391 (1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR; A01864; KIHUAR.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 28
FT NON TER 107 107
FT SEQUENCE 107 AA; 11703 MW; ELBFODF9844C3346 CRC64;

Query Match 77.7%; Score 426.5; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 1.4e-37;
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITCRASQDISHLWAWYQKSGKAPKLLIYSASSLSQSGVPSRF 62
QY 61 SSGSGVGTDFSLTISSLPEDSATYCCQANSFPYTFGQGTKEIKR 106
DB 63 SSGSGGTFTLTISLSPEDFATYCCQYNTF-FTFGPTKVDIKR 107

RESULT 4
KVLR HUMAN STANDARD; PRT; 108 AA.
ID KVLR HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
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FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match
Best Local Similarity 77.2%; Score 424; DB 1; Length 108;
Matches 82; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHQHQPAPKLLIYASASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITCRASQGISWLAHQHQPAPKLLIYASASSLSQGVPSRF 62

QY 61 SSGSGYGTDFSLTISLQFEDSATYYCCQANSFPYTFGGTKVEIKR 106
Db 63 SSGSGGTFTLTLSLQFEDPATYYCLOYSSFFTFGGTKVEIKR 108

RESULT 5
KV1W HUMAN STANDARD; PRT; 129 AA.
ID KV1W HUMAN
AC P04471
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110
FT NON TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match
Best Local Similarity 80.0%; Score 424; DB 1; Length 129;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHQHQPAPKLLIYASASSLSQGVPSRF 60
Db 25 QMTQSPSSLSASVGDRTVITCRASQGISWLAHQHQPAPKLLIYASASSLSQGVTSRF 84

QY 61 SSGSGYGTDFSLTISLQFEDSATYYCCQANSFPYTFGGTKVEIKR 105
Db 85 SSGSGGTFTLTLSLQFEDSATYYCCQSYSTLTITFGGTRLEIKR 129

RESULT 6
KV1G HUMAN STANDARD; PRT; 108 AA.
ID KV1G HUMAN
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match
Best Local Similarity 77.0%; Score 423; DB 1; Length 108;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHQHQPAPKLLIYASASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITCRASQGISWLAHQHQPAPKLLIYASASSLSQGVPSRF 62

QY 61 SSGSGYGTDFSLTISLQFEDSATYYCCQANSFPYTFGGTKVEIKR 106
Db 63 SSGSGGTFTLTLSLQFEDPATYYCLOYSSFFTFGGTKVEIKR 108

RESULT 7
KV1H HUMAN STANDARD; PRT; 108 AA.
ID KV1H HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; K1HUKU.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 77.0%; Score 423; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 3.4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSGVDRVTITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVSRF 60
Db 3 QMTQSPSLASVGDRTITCRASQSISSYLSWYQKPKAPQVLLIYAASLPSGVSRF 62
Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFQGGTKVEIKR 106
Db 63 SGSGYGTDFSLTISLQPEDSATYCCQNYITPTSFQGGTKRVEIKR 108

RESULT 8
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01598.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
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RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
RL Biochemistry 9:3189-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; K1HUEU.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.3%; Score 419; DB 1; Length 108;
Best Local Similarity 76.2%; Pred. No. 8.8e-37;
Matches 80; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSGVDRVTITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVSRF 60
Db 3 QMTQSPSLASVGDRTITCRASQSISSYLSWYQKPKAPKLLIYKASLSQGVSRF 62
Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFQGGTKVEIKR 105
Db 63 IGSGSGTFTLTISLQPEDSATYCCQYNSDSKMFQGGTKVEIKR 107

RESULT 9
KVIL HUMAN
ID KVIL HUMAN STANDARD; PRT; 108 AA.
AC P01604.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01870; K1HUKU.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DOMAIN 108 119 BY SIMILARITY.
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D9054E98 CRC64;

Query Match 76.3%; Score 419; DB 1; Length 108;
Best Local Similarity 73.6%; Pred. No. 8.8e-37;
Matches 78; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRVTITCRASQGISWLAHQHQPQKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSPQASVGDVRVTITCRASQISNIWLAHYQKPEKAPKLLIYKASTLETGVPSRF 62
QY 61 SGGSGYGTDFSLTISLQFDSATYCCQANSFPYTFGGTKVEIKR 106
DB 63 SGGSGGTFTTINSLPDDEATYCCQYSRYPYTFGGTKLIDIKR 108

RESULT 10
KV10 HUMAN
ID KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hillechmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type I-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURF.
DR PDB; 1REI; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BWV; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

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FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 75.8%; Score 416; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 1.8e-36;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRVTITCRASQGISWLAHQHQPQKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSPQASVGDVRVTITCRASQISNIWLAHYQKPEKAPKLLIYKASTLETGVPSRF 62
QY 61 SGGSGYGTDFSLTISLQFDSATYCCQANSFPYTFGGTKVEIKR 106
DB 63 SGGSGGTFTTINSLPDDEATYCCQYSRYPYTFGGTKLIDIKR 108

RESULT 11
KV18 HUMAN
ID KV18 HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RX X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlihammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

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CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR; A91653; KIHUAD.  
 DR PDB; 1JUV5; 30-JAN-02.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6B9 CRC64;  
 Query Match 75.2%; Score 413; DB 1; Length 108;  
 Best Local Similarity 75.5%; Pred. No. 3.7e-36;  
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60  
 DB 3 QMTQSPSLSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYDASNLGSGVPSRF 62  
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106  
 DB 63 SGSGGAHFTTISLQPEDATYCCQYDYLPLPTFGGTKVEIKR 108  
 RESULT 12  
 KWIM HUMAN  
 ID KVIM HUMAN STANDARD; PRT; 108 AA.  
 AC P01605;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Lay.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77038198; PubMed=824717;  
 RA Capra J.D., Klapper D.G.;  
 RT "Complete amino acid sequence of the variable domains of two human  
 IgM anti-gamma globulins (Lay/Pom) with shared idiotypic  
 specificities";  
 RL Scand. J. Immunol. 5:677-684(1976)  
 CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS  
 CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,  
 WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 GLOBULIN ACTIVITY.  
 DR PIR; A01871; KIHULY.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DISULFID 23 88  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6B9 CRC64;  
 Query Match 75.2%; Score 413; DB 1; Length 108;  
 Best Local Similarity 75.5%; Pred. No. 3.7e-36;  
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60  
 DB 3 QMTQSPSLSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYDASNLGSGVPSRF 62  
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106  
 DB 63 SGSGGAHFTTISLQPEDATYCCQYDYLPLPTFGGTKVEIKR 108  
 RESULT 13  
 KWIE HUMAN  
 ID KVIE HUMAN STANDARD; PRT; 108 AA.  
 AC P01597;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region DEE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72053133; PubMed=5124396;  
 RA Milstein C.P., Deverson E.V.;  
 RT "The amino acid sequence of a human kappa light chain.";  
 RL Biochem. J. 123:945-958(1971)  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01865; KIHUDE.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DISULFID 23 88  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;  
 Query Match 74.3%; Score 408; DB 1; Length 108;  
 Best Local Similarity 72.6%; Pred. No. 1.2e-35;  
 Matches 77; Conservative 15; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60  
 DB 3 ZMTQSPSLSASVSGDRVTITCRAGQSVNKYLNWYQKPGKAPKLLIYFAASLSKSGVPSRF 62  
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106

FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108  
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;  
 Query Match 74.7%; Score 410; DB 1; Length 108;  
 Best Local Similarity 72.6%; Pred. No. 7.6e-36;  
 Matches 77; Conservative 16; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYSASSLSQSGVPSRF 60  
 DB 3 QMTQSPSLSASVSGDRVTITCRASQGISWLAHYQHQPCKAPKLLIYDASNLGSGVPSRF 62  
 QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106  
 DB 63 SGSGYGTDFSLTISLQPEDATYCCQYDYLPLPTFGGTKVEIKR 108



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RESULT 5
Q72473
ID Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 77.4%; Score 425; DB 4; Length 236;
Best Local Similarity 78.3%; Pred. No. 3.5e-38;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQIGSSWLAWYQHQPCKAPKLLIYSASSIQCVPSPRF 60
DB 25 QMTQSPSSLSASVGTVTITCRASQDINSIYLAWFQCKPKAPKLSIYGASSIQCVPSPRF 84

QY 61 SGSGYGTDFSLTISLQFEDSATYQCQANSFPYTFGGQTKVEIKR 106
DB 85 SGSGSGTDFTLTISLQFEDSATYQCQANSFPYTFGGQTKLEIKR 130

RESULT 7
Q72473
ID Q72473 PRELIMINARY; PRT; 107 AA.
AC Q72473;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1

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FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.0%; Score 411.5; DB 4; Length 107;
Best Local Similarity 77.4%; Pred. No. 3.9e-37;
Matches 82; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQGISLWAWQHQPGRKAPKLLIYSASSLSQGVPSRF 62

QY 61 SGSGYGTDFSLTSSLSQFEDSATYCCQANSFPYTFQGTQKVEIKR 106
Db 63 SGSGSGTDFTLISGLQAEDFATYCCQSVS-ALTFGPGTKVDIR 107

RESULT 8
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scrV).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -
DR PDB; 1C1C; 11-NAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K60; 18-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214 214
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 69.9%; Score 384; DB 11; Length 214;
Best Local Similarity 67.0%; Pred. No. 9.1e-34;
Matches 71; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 3 QLTQSPSSVASYLGERVTITTCASQDINSYLSWQPKGKSPKLLIYRANLVDGVPSRF 62

QY 61 SGSGYGTDFSLTSSLSQFEDSATYCCQANSFPYTFQGTQKVEIKR 106
Db 63 SGSGSGQDYSLTSSLSLEYDMGIYCLQYDFEFPFTGSGTKLEIKR 108

RESULT 9
Q9ULB3 PRELIMINARY; PRT; 108 AA.
AC Q9ULB3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RX Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; IWTLL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 69.6%; Score 382; DB 4; Length 108;
Best Local Similarity 65.7%; Pred. No. 6.5e-34;
Matches 69; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISLWAWQHQPGRKAPKLLIYSASSLSQGVPSRF 61
Db 4 MTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPGQAPRLIYCASTRATGIDARFS 63

QY 62 GSGYGTDFSLTSSLSQFEDSATYCCQANSFPYTFQGTQKVEIKR 106
Db 64 GSGSGTEFTLTSSLSQFEDFAVYCYQHYNWPFPGTGVKDIKR 108

RESULT 10
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP STRAIN=C2CH II; TISSUE=Breast tumor;
RX MEDLINE=C2CH II; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.G., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.W., Hong L.,
RA Datschenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Carninci P., Prange C.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Besak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

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Q8VJ0 Q8VJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VKL9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AB02917.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 66.7%; Score 366; DB 11; Length 108;
Best Local Similarity 64.8%; Pred. No. 3.6e-32;
Matches 68; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITCRASQGISWLAHYQHCPGKAPKLLIYSASSLSQSGVPSRFS 61
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 4 MTQSQTFMTSVSGDRSVTCCKASQNVGTNVAWYQKPGQSPKALIIYSASYSGVPHRFT 63

QY 62 GSGYGTDFSLTISLQFEDSATYYCQANSFPYTFGGQTKVEIKR 106
   ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:
Db 64 GSGSGTDFLTISNVQSEDLAEYFCQYNSYPYTFGGGTKLEIKR 108
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RESULT 15
Q91WS9 Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
```

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Query Match 66.5%; Score 365; DB 11; Length 233;
Best Local Similarity 67.0%; Pred. No. 1.2e-31;
Matches 71; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHCPGKAPKLLIYSASSLSQSGVPSRFS 60
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 22 QMTQTTSLSASLGRVTITSCGSGQGIANYLWYQKPGDGTVKLLIYYTSSLHSGVPSRFS 81

QY 61 GSGYGTDFSLTISLQFEDSATYYCQANSFPYTFGGQTKVEIKR 106
   ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:
Db 82 GSGSGTDFSLTISLQFEDSATYYCQANSFPYTFGGGTKLEIKR 127

Search completed: August 8, 2004, 12:17:47
Job time : 30.0697 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 43.5242 Seconds  
(without alignments)  
688.123 Million cell updates/sec

Title: US-10-027-725A-12  
Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGRVTIT.....QQANSFPYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	527	96.0	106	5	ABG30450	Abg30450 Human IgE
2	518	94.4	233	3	AAB03713	Aab03713 Immunoglob
3	518	94.4	233	7	ADB72874	Adb72874 Human AAA
4	485	88.3	107	5	ABB07237	Abb07237 Anti-IL-4
5	484	88.2	223	6	ABJ36940	Abj36940 Anti-CD40
6	478	87.1	107	4	AAG65571	Aag65571 Amino aci
7	478	87.1	244	5	ABP45870	Abp45870 Human Bly
8	475	86.5	236	5	AAU74297	Aau74297 Anti-huma
9	474	86.3	105	5	AAO18424	Aao18424 Anti-GD2
10	468	85.2	234	7	AD228413	Ade228413 Human ant
11	467	85.1	107	4	AAU72880	Aau72880 Human ant
12	467	85.1	134	6	ABR55899	Abr55899 Human mAb
13	466	84.9	108	5	AAU76522	Aau76522 Anti-Inte
14	466	84.9	234	7	AD228429	Ade228429 Human ant
15	464.5	84.6	109	4	AAR10815	Aar10815 Human ant
16	463	84.3	107	4	AAQ93597	Aaq93597 Human ant
17	463	84.3	107	6	ABO27404	AbO27404 Anti-Rh(D
18	463	84.3	107	7	ADE28417	Ade28417 Human ant
19	462	84.2	107	4	AAU72882	Aau72882 Human ant
20	462	84.2	224	4	AAU75040	Aau75040 TRO005 Hu
21	461	84.0	107	7	AD228433	Ade228433 Human ant
22	461	84.0	132	6	ADA43065	Ada43065 Human ant
23	460	83.8	107	2	AAU54260	Aau54260 Anti-HIV
24	460	83.8	107	2	AAW01283	Aaw01283 VL region
25	460	83.8	107	3	AAU98244	Aau98244 Anti-gp12

ALIGNMENTS

RESULT 1

ABG30450

ID ABG30450 standard; protein; 106 AA.

XX

AC ABG30450;

DT 21-OCT-2002 (first entry)

XX

DE Human IgE Fab clone 100 light chain protein.

XX

KW Human; fab; antiallergic; vaccine; grass pollen; PhI p 2;

KV timothy grass pollen allergen; passive immunotherapy.

XX

OS Homo sapiens.

XX

FH Key

FT Region

FT Region

FT Region

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Aay95135 Anti-gp12  
Aab67511 Light cha  
Aaw70622 Human con  
Aay82345 Human con  
Abp61191 Human ant  
Aau74544 Human sub  
Aae28149 Human con  
Aab75043 TRO005 Hu  
Aab82890 Anti-huma  
Aar47041 Sequence  
Aaw01527 Monoclonal  
Aaw24990 Monoclonal  
Aab75044 TRO005 Hu  
Aar30764 Consensus  
Aao31100 Human A2-  
Aar54305 Anti-HIV  
Aaw01263 VL region  
Aay98224 Anti-gp12  
Aay95115 Anti-gp12  
Aag93663 Human ant

Location/Qualifiers  
1..21  
/note= "FR1 region"  
22..32  
/note= "CDR1 region"  
33..47  
/note= "FR2 region"  
48..54  
/note= "CDR2 protein"  
55..86  
/note= "FR3 region"  
87..95  
/note= "Encoded by TCT"  
96..104  
/note= "CDR2 region"  
97..104  
/note= "FR4 region"

WO200253595-A1.

11-JUL-2002.

27-DEC-2001; 2001WO-SE002908.

29-DEC-2000; 2000SE-00004892.

(PHAA ) PHARMACIA DIAGNOSTICS AB.

Flicker S, Steinberger P, Kraft D, Valenta R;

WPI; 2002-583604/62.

N-PSDB; ABK89642.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 41; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 100 light chain protein of the invention

XX Sequence 106 AA;

Query Match 96.0%; Score 527; DB 5; Length 106;  
 Best Local Similarity 97.2%; Pred. No. 5.1e-30;  
 Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITICRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60  
 Db 1 ELTQSPSSVSASVGDRTVITICRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60

QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 106  
 Db 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 106

RESULT 2  
 AAB03713  
 ID AAB03713 standard; protein; 233 AA.

XX AAB03713;

XX 04-OCT-2000 (first entry)

XX Immunoglobulin kappa amino acid sequence fragment.

XX Aortic aneurysm-associated antigen protein; AAAP; microfibrillar protein;  
 KW abdominal aortic aneurysm disease; treatment; detect; tolerance;  
 KW immunoglobulin kappa; Igk.

XX Unidentified.

XX US6048704-A.

XX 11-APR-2000.

XX 07-MAR-1997; 97US-00812586.

XX 07-MAR-1996; 96US-0012976P.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Tilson MD;

XX WPI; 2000-316895/27.

XX Isolated microfibrillar protein for alleviating abdominal aortic aneurysm  
 PT disease is purified from human aortic tissue and binds immunoreactively  
 PT with immunoglobulin.

XX Example 3; Col 29-31; 70pp; English.

XX The present invention relates to an isolated microfibrillar protein of  
 CC approximately 40kD. The protein is isolated from human aortic tissue and  
 CC binds immunoreactively with immunoglobulin purified from human abdominal  
 CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic  
 CC aneurysm-associated antigenic protein (AAAP). The protein is capable of  
 CC forming a disulphide bonded dimer. The protein is immunoreactive with  
 CC human kappa immunoglobulin. Also included in the invention are  
 CC recombinantly produced human AAA proteins. AAAP shows regions of homology  
 CC with the bovine microfibril associated glycoprotein MFAP-4 and also with  
 CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful  
 CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the  
 CC presence of AAA-associated immunoglobulin bound to the human aortic  
 CC tissue. Antibodies directed against AAAP can be used to detect AAA  
 CC disease. The recombinant protein can be used to induce tolerance to  
 CC antigenic AAA protein in the subject e.g. human. This sequence represents  
 CC an immunoglobulin kappa amino acid sequence. The sequence shares homology  
 CC with the AAAP of the invention, it was used to identify and characterise  
 CC AAAP

XX Sequence 233 AA;

Query Match 94.4%; Score 518; DB 3; Length 233;  
 Best Local Similarity 96.2%; Pred. No. 4.4e-29;  
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITICRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60  
 Db 23 ELTQSPSSVSASVGDRTVITICRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 82

QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 106  
 Db 83 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIKR 128

RESULT 3  
 ADB72874  
 ID ADB72874 standard; protein; 233 AA.

XX ADB72874;

XX 04-DEC-2003 (first entry)

XX Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.

XX Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;

XX AAA-associated immunoglobulin 40kDa protein.

XX Homo sapiens.

XX US6537769-B1.

XX 25-MAR-2003.

XX 28-MAR-2000; 2000US-00535832.

XX 07-MAR-1996; 96US-0012976P.

XX 07-MAR-1997; 97US-00812586.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Tilson MD;

XX WPI; 2003-687181/65.

XX Purified protein useful in diagnosing abdominal aortic aneurysm disease  
 PT in subject, e.g. human, contains specified amino acids.

XX Disclosure; Col 73-74; 67pp; English.

XX The present invention relates to the isolation of a protein approximately  
 CC 40kDa which is purified from human aortic tissue. The protein is  
 CC immunoreactive with abdominal aortic aneurysms (AAA)-associated

CC immunoglobulin. The protein is useful for diagnosing AAA disease in a  
 CC subject, e.g. human, by administering the protein or a composition  
 CC comprising the protein. The inventive protein is capable of forming a  
 CC disulphide-bonded dimer of 80 kDa. The present sequence of unknown  
 CC function is given in the Sequence Listing but is not mentioned elsewhere  
 CC in the specification.

XX SQ Sequence 233 AA;

Query Match 94.4%; Score 518; DB 7; Length 233;  
 Best Local Similarity 96.2%; Pred. No. 4.4e-29;  
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 60  
 |||||

Db 23 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 82  
 |||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIKR 106  
 |||||

Db 83 SGSGSGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIKR 128  
 |||||

RESULT 4

AB07237  
 ID AB07237 standard; protein; 107 AA.

XX AC AB07237;

XX DT 26-MAR-2002 (first entry)

XX DE Anti-IL-4 and IL-13 receptors MAb 63 light chain variable region.

XX KW Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;  
 KW antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic;  
 KW antischlicking; immunosuppressive; tuberculostatic; ophthalmological;  
 XX IL-13; antianemic; antithyroid.

XX CS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 24..34  
 /note= "complementarity determining region (CDR) 1"

FT Region 50..56  
 /note= "complementarity determining region (CDR) 2"

FT Region 89..97  
 /note= "complementarity determining region (CDR) 3"

XX W0200192340-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US017094.

XX PR 26-MAY-2000; 2000US-00579808.

XX PR 19-SEP-2000; 2000US-0065343.

XX PR 15-FEB-2001; 2001US-00785934.

XX PR 01-MAY-2001; 2001US-00847816.

XX (IMV ) IMMUNEX CORP.

XX Plueneke JD;

XX WPI; 2002-114332/15.

XX N-PSDB; ABA94337.

XX Novel human antibody which binds human interleukin (IL)-4 receptor and is  
 PT capable of inhibiting IL-4 induced biological activity, functions as IL-4  
 PT antagonist and is useful for treating septic arthritis, scleroderma.

XX Claim 3; Page 82; 85pp; English.

XX The invention relates to a human antibody (an interleukin (IL)-4

CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of

CC inhibiting an IL-4-induced biological activity. (I) is also useful for  
 CC inhibiting both IL-4-induced biological activity and IL-13-induced  
 CC biological activity in vivo in a human, and for treating septic arthritis  
 CC in a human afflicted with septic arthritis. (I) is also used for treating  
 CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,  
 CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric  
 CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,  
 CC inflammatory bowel disease, other disorders of the digestive system in  
 CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the  
 CC gastrointestinal tract), conditions in which IL-4-induced barrier  
 CC disruption plays a role (e.g. conditions characterized by decreased  
 CC epithelial barrier function in the lung or gastrointestinal tract),  
 CC scleroderma, hypertrophic scarring, Whipple's disease, benign prostate  
 CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to  
 CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-  
 CC Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,  
 CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,  
 CC Barrett's esophagus, autoimmune uveitis, tuberculous, nephrosis,  
 CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering  
 CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4  
 CC antagonists also find use as adjuvants to allergy immunotherapy and as  
 CC vaccine adjuvants, especially when directing the immune response toward a  
 CC TH1 response would be beneficial in treating or preventing the disease.  
 CC The present sequence represents an anti-IL-4 receptor and anti-IL-13  
 CC receptor monoclonal antibody (MAB) 63 light chain variable region

XX SQ Sequence 107 AA;

Query Match 88.3%; Score 485; DB 5; Length 107;  
 Best Local Similarity 88.6%; Pred. No. 4.6e-27;

Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 60  
 :|||||

Db 3 QMTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPAPKLLIYSASLSQGVPSRF 62  
 :|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIK 105  
 |||||

Db 63 SGSGSGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIK 107  
 |||||

RESULT 5

ABJ36940

ID ABJ36940 standard; protein; 223 AA.

XX AC ABJ36940;

XX DT 01-MAY-2003 (first entry)

XX DE Anti-CD40 monoclonal antibody related protein SEQ ID No 66.

XX KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;  
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;  
 KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;  
 KW immunoactivator; anti-tumour agent; immunosuppressant; allergy;  
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.

XX OS Unidentified.

XX WO200288186-A1.

XX PD 07-NOV-2002.

XX PF 26-APR-2002; 2002WO-JP004292.

XX PR 27-APR-2001; 2001WO-US013672.

XX PR 11-MAY-2001; 2001JP-0042462.

XX PR 05-OCT-2001; 2001JP-00310535.

XX PR 26-OCT-2001; 2001US-00040244.

XX (KIRI ) KIRIN BEER KK.

XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;

XX WPI; 2003-120463/11.  
 DR N-PSDB; ABT31882.  
 XX  
 PT Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,  
 PT or functional fragment, is useful in the treatment of e.g. autoimmune  
 PT diseases or cancer.  
 XX  
 XX Claim 15; Page 60; 94pp; Japanese.  
 XX  
 XX The invention relates to an antibody to human CD40, or its functional  
 CC fragment, has at least one of the following properties: acting on  
 CC dendritic cells to produce IL-12 in the presence of LPS  
 CC (lipopolysaccharide) and IFN $\gamma$  (interferon gamma); acting on dendritic  
 CC cells to activate maturation of the dendritic cells with high G28-5  
 CC antibody; and activating CD95 expression with high G28-5 antibody against  
 CC B cell line. Such antibodies or functional fragments can be used as  
 CC immunoadjuvants, anti-tumour agents, immunosuppressants, and as remedies  
 CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors  
 CC syndrome. This sequence represents a protein relating to the anti-CD40  
 CC monoclonal antibody of the invention  
 XX  
 XX Sequence 223 AA;  
 SQ

Query Match 88.2%; Score 484; DB 6; Length 223;  
 Best Local Similarity 87.7%; Pred. No. 1e-26; Indels 0; Gaps 0;  
 Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGDRTVTITCRASQGISWLAHYQHOPGKAPKLLIYASLSQSGVPSRF 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 25 QMTQSPSSVSASVGDRTVTITCRASQGISWLAHYQHOPGKAPKLLIYAGSLQSGVPSRF 84  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 SGSGYGDFSLTISLQPEDSATYCCQANSPFYTFGGTKVEIKR 106  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 85 SGSGYGFDTLTISLQPEDPATYCCQANSPFYTFGGTKVEIKR 130  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6  
 AAG65571  
 ID AAG65571 standard; protein; 107 AA.

AC AAG65571;  
 XX  
 DT 30-NOV-2001 (first entry)  
 XX  
 XX Amino acid sequence of protein seq Id No. 96.  
 DE  
 XX Gene library; immunoglobulin; antibody library; human.  
 KW  
 XX Homo sapiens.  
 OS

XX WO200162907-A1.  
 XX

PD 30-AUG-2001.  
 XX

PF 22-FEB-2001; 2001WO-JP001298.  
 XX

XX 22-FEB-2000; 2000JP-00050543.  
 XX

XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.  
 XX

XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;  
 PI Okuno Y, Shiraki K;  
 XX

XX WPI; 2001-565420/63.  
 DR

DR N-PSDB; AAH47735.  
 DR

XX Producing gene libraries and antibody libraries, involves selecting a  
 PT light chain that binds to a heavy chain product to produce a functional  
 PT formation, and producing a gene library of the light chain variable  
 PT regions.  
 XX

PS Examples; p 172; 181pp; Japanese.

XX The invention relates to producing gene libraries, comprising  
 CC immunoglobulin light and heavy variable region. The method involves  
 CC selecting light chain that binds with the heavy chain product to produce  
 CC a functional conformation, producing a gene library comprising a  
 CC collection of these light chain variable genes, and combining with gene  
 CC library of heavy chain variable genes. The method is used for production  
 CC of gene and antibody libraries  
 XX  
 XX Sequence 107 AA;  
 SQ

Query Match 87.1%; Score 478; DB 4; Length 107;  
 Best Local Similarity 86.6%; Pred. No. 1.4e-26;  
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVTITCRASQGISWLAHYQHOPGKAPKLLIYASLSQSGVPSRF 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 3 QMTQSPSSVSASVGDRTVTITCRASQGISWLAHYQHOPGKAPKLLIYAGSLQSGVPSRF 62  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 SGSGYGDFSLTISLQPEDSATYCCQANSPFYTFGGTKVEIK 105  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 63 SGSGYGFDTLTISLQPEDPATYCCQANSPFYTFGGTKVEIK 107  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7  
 ABP45870  
 ID ABP45870 standard; protein; 244 AA.

AC ABP45870;  
 XX

XX 19-AUG-2002 (first entry)  
 DT

XX Human Blys binding scFv SEQ ID 1881.  
 XX

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.  
 OS

XX WO200202641-A1.  
 XX

XX 10-JAN-2002.  
 XX

XX 15-JUN-2001; 2001WO-US019110.  
 XX

XX 16-JUN-2000; 2000US-0212210P.  
 PR

PR 17-OCT-2000; 2000US-0240816P.  
 PR

PR 16-MAR-2001; 2001US-0276248P.  
 PR

PR 21-MAR-2001; 2001US-0277379P.  
 PR

PR 25-MAY-2001; 2001US-0293499P.  
 XX

XX (HUNA-) HUMAN GENOME SCI INC.  
 PA

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI; 2002-114799/15.  
 XX

DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 PT

PS Claim 1; Page 2646-2647; 3148pp; English.  
 XX

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to





PS Claim 3; Fig 7A; 14pp; German.  
XX  
CC The present invention relates to a composition for treating tumours  
CC positive for disialoganglioside GD2 which is based on human antibody  
CC fragments that activate the immune system against GD2, specifically by  
CC inducing anti-GD2 antibodies. The composition can be used in the  
CC treatment of neuroblastoma and melanoma. The present sequence is an anti-  
CC GD2 antibody light chain  
XX  
SQ Sequence 105 AA;  
Query Match 86.3%; Score 474; DB 5; Length 105;  
Best Local Similarity 89.5%; Pred. No. 2.7e-26;  
Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 60  
Db 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASLSQSGVPSRF 60  
Qy 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPVTFGGTKVEIK 105  
Db 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPVTFGGTKVEIK 105  
RESULT 10  
ADE28413  
ID ADE28413 standard; protein; 234 AA.  
XX  
AC ADE28413;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human anti-CD40 antibody 10-8-3 variable region light chain protein.  
XX  
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; variable region light chain; 10-8-3.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040170-A2.  
XX  
PD 15-MAY-2003.  
XX  
PP 08-NOV-2002; 2002WO-US036107.  
XX  
PR 09-NOV-2001; 2001US-0348980P.  
XX  
PA (PFIZ ) PFIZER PROD INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX  
DR WPI; 2003-441521/41.  
DR N-PSDB; ADE28412.  
XX  
PT New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.  
XX  
PS Claim 1; SEQ ID NO 20; 177pp; English.  
XX  
CC The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene

CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody variable region light chain protein of the invention.  
XX  
SQ Sequence 234 AA;  
Query Match 85.2%; Score 468; DB 7; Length 234;  
Best Local Similarity 86.8%; Pred. No. 1.4e-25;  
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 60  
Db 23 QMTQSPSSVSASVGDRTVITTCRASQPTISSWLAHYQKPKAPKLLIYSASLSQSGVPSRF 82  
Qy 61 SGSGYGTDFSLTISLQFDSATYCCOANSFPVTFGGTKVEIKR 106  
Db 83 SGSGYGTDFSLTISLQFDSATYCCOANSFPVTFGGTKVEIKR 128  
RESULT 11  
AAB72880  
ID AAB72880 standard; protein; 107 AA.  
XX  
AC AAB72880;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Human anti-HER2/neu antibody 3-F2 light chain.  
XX  
KW Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;  
KW 1-D2; 2-E8; growth factor receptor.  
XX  
OS Homo sapiens.  
XX  
PN WO200109187-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 25-JUL-2000; 2000WO-US020272.  
XX  
PR 29-JUL-1999; 99US-0146313P.  
PR 10-MAR-2000; 2000US-0188539P.  
XX  
PA (MEDA-) MEDAREX INC.  
XX  
PI Keller T, Deo Y;  
XX  
DR WPI; 2001-168699/17.  
DR N-PSDB; AAF75586.  
XX  
PT New human monoclonal antibody that specifically binds to growth factor  
PT receptor HER2/neu, for treating, preventing or diagnosing diseases  
PT characterized by aberrant HER2/neu expression e.g. cancers.  
XX  
PS Disclosure; Page 104-105; 113pp; English.  
XX  
CC The present invention provides the protein and coding sequences for human  
CC monoclonal antibodies which bind specifically to the HER2/neu growth  
CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2  
CC and 2-E8. They can be used in the immunotherapy-based treatment and  
CC prognosis of cancers, particularly adenocarcinomas such as salivary  
CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,  
CC and ovarian cancer. The present sequence is part of an antibody of the  
CC invention  
XX  
SQ Sequence 107 AA;  
Query Match 85.1%; Score 467; DB 4; Length 107;  
Best Local Similarity 85.7%; Pred. No. 8.5e-26;  
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF 60  
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQKPKAPKLLIYAASLSQSGVPSRF 62

QY 61 SSGSGYGTDFSLTISLQPEDSATYCCQANSFYTFGQGTKEIK 105  
Db 63 SSGSGIDFTLTISLQPEDFATYCCQXNSPYTFGQGTKEIK 107

## RESULT 12

ABR55899  
ID ABR55899 standard; protein; 134 AA.

XX ABR55899;  
XX 02-SEP-2003 (first entry)  
XX Human mAb 4C2 light chain VJ region.

XX Mitochondrial antigen; autoantibody; biliary cirrhosis; transgenic;  
KW monoclonal antibody; mAb.

OS Homo sapiens.

PN WO200276406-A2.

XX 03-OCT-2002.

XX 27-MAR-2002; 2002WO-US009694.

XX 27-MAR-2001; 2001US-0279052P.

XX 21-SEP-2001; 2001US-0323920P.

XX (GERS/) GERSHWIN M E.

XX Gershwin ME;

XX WPI; 2003-018951/01.

XX New anti-mitochondrial antigen specific human monoclonal antibodies from  
PT patients with primary biliary cirrhosis (PBC), useful as a diagnostic  
PT reagent, or as a reagent for screening antagonists for treating patients  
PT with PBC.

XX Claim 22; Page 102; 150pp; English.

XX The invention relates to an isolated human antibody or its antigen-  
CC binding portions, which binds a mitochondrial antigen bound by a human  
CC autoantibody found in patients with primary biliary cirrhosis. The  
CC antibody is useful as a diagnostic reagent, e.g. for monitoring whether a  
CC transplanted liver in a patient with primary biliary cirrhosis, is  
CC expressing a mitochondrial antigen bound by an autoantibody. The antibody  
CC is also useful for purifying an antigen to which it binds, for producing  
CC an anti-idiotypic antibody to it, or as a reagent to screen for  
CC antagonists to it, either in vivo or in vitro. The antagonist is useful  
CC for treating a patient with primary biliary cirrhosis, or for  
CC prophylactically treating a patient about to have primary biliary  
CC cirrhosis. The present sequence represents the VJ region of the light  
CC chain of an anti-mitochondrial antigen human mAb (monoclonal antibody)  
CC 4C2

XX Sequence 134 AA;

Query Match 85.1%; Score 467; DB 6; Length 134;  
Best Local Similarity 87.4%; Pred. No. 1e-25;  
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 QSPSSVSASGDRVTITCRASGIGSSWLAWYQHCPGKAPKLLIYASSLQSGVPSRFGS 63  
Db 1 QSPSSVSASGDRVTITCRASGIGSSWLAWYQHCPGKAPKLLIYASSLQSGVPSRFGS 60

QY 64 GYCTDFSLTISLQPEDSATYCCQANSFYTFGQGTKEIKR 106

Db 61 GSGTDFLTISLQPEDFATYCCQANSFYTFGQGTKEIKR 103

## RESULT 13

AAU76522  
ID AAU76522 standard; protein; 108 AA.

XX AAU76522;

XX 05-JUN-2002 (first entry)

XX Anti-Interleukin-12 (IL-12) antibody variable region #2.

XX Human; antibody; anti-interleukin-12; CDR; heavy chain; circulatory;  
KW complementarity determining region; neuroprotective; antipsoriatic;  
KW immunostimulant; cytostatic; anti-microbial; psoriasis; infection;  
KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;  
KW neurological disorder.

XX Homo sapiens.

XX WO200212500-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024720.

XX 07-AUG-2000; 2000US-0223358P.

XX 29-SEP-2000; 2000US-0236827P.

XX 01-AUG-2001; 2001US-00920262.

XX (CENZ ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;

XX WPI; 2002-257482/30.

XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL  
PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as  
PT other for treating immune, infectious, malignant or neurological  
PT disorders.

XX Claim 1; Page 93-94; 96pp; English.

XX The invention relates to novel isolated mammalian anti-interleukin-12 (IL  
CC -12) antibodies. The antibodies comprise at least one complementarity  
CC determining region (CDR) of a heavy or light chain, a heavy chain or  
CC light chain variable region, or a heavy chain or light chain constant  
CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or  
CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.  
CC The antibodies are also useful for treating immune, cardiovascular,  
CC infectious, malignant or neurological disorders or diseases. The present  
CC sequence represents the amino acid sequence of human anti-interleukin-12  
CC (IL-12) antibody variable region #2

XX Sequence 108 AA;

Query Match 84.9%; Score 466; DB 5; Length 108;  
Best Local Similarity 84.9%; Pred. No. 1e-25;  
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASGDRVTITCRASGIGSSWLAWYQHCPGKAPKLLIYASSLQSGVPSRF 60

Db 3 QMTQSPSSLSASGDRVTITCRASGIGSSWLAWYQHCPGKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYGTDFSLTISLQPEDSATYCCQANSFYTFGQGTKEIKR 106

Db 63 SSGSGTDFLTISLQPEDFATYCCQVNTYPTTFGQGTKEIKR 108

## RESULT 14

ADE28429  
ID ADE28429 standard; protein; 234 AA.

XX ADE28429;

DT 29-JAN-2004 (first entry)  
 XX Human anti-CD40 antibody 21-2-1 variable region light chain protein.  
 DE  
 XX  
 XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
 KW human; variable region light chain; 21-2-1.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003040170-A2.  
 FN  
 XX  
 XX 15-MAY-2003.  
 PD  
 XX  
 XX 08-NOV-2002; 2002WO-US036107.  
 PF  
 XX  
 XX 09-NOV-2001; 2001US-0348980P.  
 FR  
 XX  
 XX (PFIZ ) PFIZER PROD INC.  
 PA  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX  
 XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
 PI  
 XX WPI; 2003-441521/41.  
 XX  
 XX N-PSDB; ADE28428.  
 DR  
 XX  
 XX New chimeric or human monoclonal antibody or its antigen-binding portion  
 PT that specifically binds to and activates human CD40, useful for enhancing  
 PT an immune response in a human, or treating cancer, HIV, neutropenia or  
 PT viral infections.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 36; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or  
 CC its antigen-binding portion that specifically binds to and activates  
 CC human CD40. The anti-CD40 antibody of the invention demonstrates  
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
 CC activities and may be useful for treating a hyperproliferative disorder  
 CC such as cancer, viral and bacterial infection or genetic, primary or  
 CC combined immunodeficiency conditions including neutropenia or HIV  
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
 CC in a biological sample in vitro or in vivo, as well as during gene  
 CC therapy procedures. The current sequence is that of the human anti-CD40  
 CC antibody variable region light chain protein of the invention.

XX Sequence 234 AA;

Query Match 84.9%; Score 466; DB 7; Length 234;  
 Best Local Similarity 85.8%; Pred. No. 2e-25;  
 Matches 91; Conservative 6; Mismatches 9; Indels 9; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRF 60  
 Db 23 QMTQSPSSVSASVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYTASTLOSQGVPSRF 82  
 Qy 61 SGSGYGTDFSLITLTISSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106  
 Db 83 SGSGSGTDFTLITLTISSLOFEDFATYCCQANIFPLTFGGTKVEIKR 128

RESULT 15

AAE10815  
 ID AAE10815 standard; protein; 109 AA.

XX  
 AC AAE10815;

XX 18-DEC-2001 (first entry)

XX Human antibody CAT-212 light chain variable domain.

XX Human; eotaxin; CAT-212; antibody; light chain variable region; VL;  
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;

KW vasotropic; conjunctivitis; allergic colitis; psoriasis; pemphigoid;  
 KW eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;  
 KW inflammatory bowel disease; gastroenteritis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..2  
 FT /note= "Encoded by ACATC"  
 FT  
 XX

PN WO200166754-A1.

XX 13-SEP-2001.

XX 02-MAR-2001; 2001WO-GB000927.

XX 03-MAR-2000; 2000US-0187246P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Vaughan TJ, Wilton AJ, Smith S;

XX WPI; 2001-589944/66.

XX N-PSDB; AAD18149.

XX Human antibodies against eotaxin useful for treating asthma, eczema and  
 CC other atopic diseases, comprises an antibody variable heavy or variable  
 CC light domain from CAT-212 or from complementary determining regions.

XX Claim 1; Page 102; 107pp; English.

XX The invention relates to a specific binding member which binds to human  
 CC eotaxin. The binding member comprises an antibody variable heavy  
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL  
 CC domain comprising one or more VH/VL complementary determining regions  
 CC (CDRs). Eotaxin is a chemottractant protein that binds to a specific  
 CC receptor which is expressed predominantly on eosinophils. The binding  
 CC member is useful for neutralising eotaxin, which is useful in treating  
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,  
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-  
 CC mediated diseases; for treating skin and other atopic conditions such as  
 CC psoriasis, pemphigoid, wells' syndrome, cellulitis, drug eruptions; as  
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/  
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin  
 CC syndrome, Churg-Strassers syndrome. The present sequence is human antibody  
 CC CAT-212 light chain variable domain (VL) which binds to eotaxin

XX Sequence 109 AA;

Query Match 84.6%; Score 464.5; DB 4; Length 109;  
 Best Local Similarity 86.0%; Pred. No. 1.3e-25;  
 Matches 92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRF 60  
 Db 3 QMTQSPSSVSASVGDRTVITCRASQGISWLAHYOHOPGKAPKLLIYTASTLOSQGVPSRF 62  
 Qy 61 SGSGYGTDFSLITLTISSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106  
 Db 63 SGSGSGTDFTLITLTISSLOFEDFATYCCQASSFPITFGGTRLEIKR 109

Search completed: August 8, 2004, 12:13:50  
 Job time : 45.5242 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 35.8152 Seconds  
(without alignments)  
928.389 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGDRTVT.....QQANSFPYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

#### Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	106	14	US-10-027-725A-12
2	484	88.2	223	16	US-10-693-629-66
3	482	87.8	107	15	US-10-309-762-159
4	481	87.6	107	12	US-10-292-088-105
5	479	87.2	107	15	US-10-309-762-62
6	479	87.2	107	15	US-10-309-762-164
7	478	87.1	107	15	US-10-309-762-61
8	478	87.1	107	15	US-10-309-762-64
9	478	87.1	244	10	US-09-880-748-1881
10	478	87.1	244	12	US-10-293-418-1881
11	475	86.5	236	9	US-09-859-053-30
12	474	86.3	107	14	US-10-041-860-43
13	474	86.3	107	14	US-10-041-860-218
14	474	86.3	107	16	US-10-665-383-64
15	473.5	86.2	106	15	US-10-309-762-84

16	472	86.0	107	15	US-10-309-762-60	Sequence 60, Appl
17	472	86.0	107	15	US-10-309-762-63	Sequence 63, Appl
18	468.5	85.3	108	14	US-10-041-860-357	Sequence 357, App
19	468	85.2	234	12	US-10-292-088-24	Sequence 24, Appl
20	466	84.9	108	10	US-09-920-262A-8	Sequence 8, Appl
21	466	84.9	234	12	US-10-292-088-48	Sequence 48, Appl
22	464.5	84.6	109	9	US-09-798-058-4	Sequence 4, Appl
23	464.5	84.6	109	15	US-10-220-418-4	Sequence 4, Appl
24	464	84.5	107	12	US-10-269-711-17	Sequence 17, Appl
25	464	84.5	107	12	US-10-269-711-25	Sequence 25, Appl
26	464	84.5	107	12	US-10-269-711-29	Sequence 29, Appl
27	463	84.3	107	10	US-09-848-798-40	Sequence 40, Appl
28	463	84.3	107	12	US-10-292-088-20	Sequence 20, Appl
29	462.5	84.2	106	14	US-10-040-244-17	Sequence 17, Appl
30	462	84.2	106	16	US-10-027-725A-10	Sequence 10, Appl
31	462	84.2	108	16	US-10-408-901-20	Sequence 20, Appl
32	462	84.2	214	16	US-10-408-901-44	Sequence 44, Appl
33	461	84.0	107	12	US-10-292-088-44	Sequence 44, Appl
34	461	84.0	108	16	US-10-408-901-12	Sequence 12, Appl
35	461	84.0	132	16	US-10-469-304-23	Sequence 23, Appl
36	461	84.0	214	16	US-10-408-901-36	Sequence 36, Appl
37	460	83.8	107	12	US-09-948-939-13	Sequence 13, Appl
38	460	83.8	107	12	US-10-269-711-9	Sequence 9, Appl
39	460	83.8	107	12	US-10-269-711-13	Sequence 13, Appl
40	460	83.8	107	14	US-10-016-986-104	Sequence 104, App
41	460	83.8	108	9	US-09-056-160B-12	Sequence 12, Appl
42	460	83.8	108	11	US-09-795-798-3	Sequence 3, Appl
43	460	83.8	108	14	US-10-234-671-12	Sequence 12, Appl
44	460	83.8	109	9	US-09-811-123-6	Sequence 6, Appl
45	460	83.8	110	14	US-10-044-896-4	Sequence 4, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-027-725A-12  
; Sequence 12, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-12

Query Match 100.0%; Score 549; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.8e-42;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ELTQSPSSVSASVGDRTVTTCRASOGISSLAWYQHQPQKAPKLLIYGSASSIQSGVPSRF	60
Db	1	ELTQSPSSVSASVGDRTVTTCRASOGISSLAWYQHQPQKAPKLLIYGSASSIQSGVPSRF	60
Qy	61	SGSGYGTDFSLTISSLFQEDSATYCCQANSFPYTFGGTKVEIKR	106
Db	61	SGSGYGTDFSLTISSLFQEDSATYCCQANSFPYTFGGTKVEIKR	106

##### RESULT 2

US-10-693-629-66  
; Sequence 66, Application US/10693629  
; Publication No. US20040120948A1  
; GENERAL INFORMATION:

```

; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-693-629-66

Query Match      88.2%; Score 484; DB 16; Length 223;
Best Local Similarity 87.7%; Pred. No. 1.1e-35;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
Db 25 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAGSLQSGVPSRF 84

Qy 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106
Db 85 SGSGFGDTFLTITSSLPEDFATYCCOANSFPYTFQGTKEIKR 130

RESULT 3
US-10-309-762-159
; Sequence 159, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-159

Query Match      87.8%; Score 482; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 8e-36;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASSLSQGVPSRF 62

us-10-027-725a-12.rapb

Qy 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIK 105
Db 63 SGSGSGTDFLTITSSLPEDFATYCCOANSFPYTFQGTREIK 107

RESULT 4
US-10-292-088-105
; Sequence 105, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-105

Query Match      87.6%; Score 481; DB 12; Length 107;
Best Local Similarity 89.5%; Pred. No. 9.8e-36;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASSLSQGVPSRF 62

Qy 61 SGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFQGTKEIK 105
Db 63 SGSGSGTDFLTITSSLPEDFATYCCOANSFPYTFQGTKEIK 107

RESULT 5
US-10-309-762-62
; Sequence 62, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-62

Query Match      87.2%; Score 479; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-35;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASSLSQGVPSRF 62
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QY 61 SSGSGYTDFTLTISSILOPDSATYYCCQANSPPYTFGGTKVEIK 105

Db 63 SSGSGSTDTFTLTISSILOPEDATYYCCQANSPPYTFGGTKVDIK 107

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RESULT 6
US-10-309-762-164
; Sequence 164, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Jean
; APPLICANT: Hands, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-164

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[illegible]

```

RESULT 7
US-10-309-762-61
; Sequence 61, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX-027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-61

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Qy 1. ELTQSPSSVASVGDRVTITCRASQGISSLAWYHQPGKAPKLLIYSASSLQSGVPSRF 60

Db 3 QMTQPSSVASGVDRVTITCRASQGISLWAFQKPGKAPKLLIYAASSIQSGVPSRF 62

Qy 61 SSGSGYGTDFSLTISIQFEDSATYYCOQANSPYTFGQTKVEIK 105

Db 63 SSGSGTDFTLTISLQPDFTATYYCOQANSPYTFGQTRLEIK 107

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RESULT 8
US-10-309-762-64
; Sequence 64, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Hands, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; FILE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-64

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QY	Db	QY	Db
1	3	61	63
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60	62	105	107

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RESULT 9
US-09-880-748-1881
/ Sequence 1881, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1881
/ LENGTH: 244
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1881

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Query Match 87.1%; Score 478; DB 10; Length 244;

Best Local Similarity 88.6%; Pred. No. 4.1e-35;  
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDVRTTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLQSGVPSRF 61  
Db 140 MTQSPSTLSASVGDVRTTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLQSGVPSRF 199

QY 62 GSGYGTDFSLTITSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 106  
Db 200 GSGSGTDFTLTITSSLOPEDFATYCCQANSFPPLTFGGTKVEIKR 244

RESULT 10  
US-10-293-418-1881  
; Sequence 1881, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1881  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1881

Query Match 87.1%; Score 478; DB 12; Length 244;  
Best Local Similarity 88.6%; Pred. No. 4.1e-35;  
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDVRTTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLQSGVPSRF 61  
Db 140 MTQSPSTLSASVGDVRTTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLQSGVPSRF 199

QY 62 GSGYGTDFSLTITSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 106  
Db 200 GSGSGTDFTLTITSSLOPEDFATYCCQANSFPPLTFGGTKVEIKR 244

RESULT 11  
US-09-859-053-30  
; Sequence 30, Application US/09859053  
; Patent No. US20020102658A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, No. US20020102658A1uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILTM AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859,053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-859-053-30

Query Match 86.5%; Score 475; DB 9; Length 236;  
Best Local Similarity 88.7%; Pred. No. 7.4e-35;  
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRTTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLQSGVPSRF 60  
Db 25 QMTQSPSSVSASVGDVRTTITCRASQGISRLLAHYQKPGKAPKLLIYVASSLQSGVPSRF 84  
QY 61 GSGYGTDFSLTITSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 106  
Db 85 GSGSGTDFTLTITSSLOPEDFATYCCQANSFPWTFGGTKVEIKR 130

RESULT 12  
US-10-041-860-43  
; Sequence 43, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; FILE REFERENCE: ARGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-43

Query Match 86.3%; Score 474; DB 14; Length 107;  
Best Local Similarity 87.6%; Pred. No. 4.2e-35;  
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRTTITCRASQGISWLAHYQHQPCKAPKLLIYASASSLQSGVPSRF 60  
Db 3 QMTQSPSSVSASVGDVRTTITCRASQGISWLAHYQKPGKAPKLLIYVASSLQSGVPSRF 62

QY 61 GSGYGTDFSLTITSSLOPEDSATYCCQANSFPYTFGGTKVEIK 105  
Db 63 GSGSGTDFTLTITSSLOPEDFATYCCQANSFPRTFGGTKVEIK 107

RESULT 13  
US-10-041-860-218  
; Sequence 218, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine







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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 12.6879 Seconds  
(without alignments)  
431.306 Million cell updates/sec

Title: US-10-027-725A-12  
Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGDRTVTIT.....QQANSFFYFGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/2/iaa/5B COMB.pdp:\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pdp:\*  
4: /cgn2\_6/prodata/2/iaa/6B COMB.pdp:\*  
5: /cgn2\_6/prodata/2/iaa/6C COMB.pdp:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	94.4	233	3	US-08-812-586-45
2	518	94.4	233	4	US-09-535-832A-42
3	466	84.9	109	2	US-07-934-373C-3
4	466	84.9	109	3	US-08-437-642B-3
5	466	84.9	109	4	US-08-146-206C-3
6	466	84.9	109	4	US-09-705-686-3
7	466	84.9	109	5	PCT-US93-07832-3
8	463	84.3	107	3	US-09-240-274-40
9	460	83.8	107	1	US-08-276-852-104
10	460	83.8	107	1	US-08-899-575-104
11	460	83.8	107	1	US-08-899-575-104
12	460	83.8	107	5	PCT-US95-08743-104
13	460	83.8	108	3	US-08-974-899-3
14	459	83.6	128	1	US-08-259-372A-14
15	459	83.6	128	1	US-08-468-671-14
16	457	83.2	107	1	US-08-276-852-84
17	457	83.2	107	1	US-08-899-575-84
18	457	83.2	107	1	US-08-899-575-84
19	457	83.2	107	3	US-09-240-274-175
20	457	83.2	107	3	US-09-240-274-175
21	457	83.2	107	5	PCT-US95-08743-84
22	456	83.1	107	3	US-09-240-274-156
23	456	83.1	109	3	US-09-157-370-3
24	455	82.9	107	2	US-07-934-373C-18
25	455	82.9	107	3	US-08-437-642B-18
26	455	82.9	107	4	US-08-146-206C-18
27	455	82.9	107	4	US-09-648-067A-14

28 455 82.9 107 4 US-09-705-686-18 Sequence 18, Appl  
29 455 82.9 107 5 PCT-US93-07832-18 Sequence 18, Appl  
30 454 82.7 109 4 US-09-025-769B-28 Sequence 28, Appl  
31 454 82.7 109 4 US-09-025-769B-43 Sequence 43, Appl  
32 453 82.5 108 2 US-08-552-816A-4 Sequence 4, Appl  
33 452 82.3 107 1 US-08-276-852-105 Sequence 105, App  
34 452 82.3 107 1 US-08-899-575-105 Sequence 105, App  
35 452 82.3 107 5 PCT-US95-08743-105 Sequence 105, App  
36 452 82.3 107 3 US-09-240-274-179 Sequence 179, App  
37 451 82.1 107 3 US-08-599-226-1 Sequence 1, Appl  
38 450 82.0 107 3 US-09-125-098-1 Sequence 1, Appl  
39 450 82.0 107 4 US-09-540-018-1 Sequence 32, Appl  
40 449.5 81.9 108 3 US-09-240-274-32 Sequence 82, Appl  
41 449.5 81.9 108 3 US-08-276-852-82 Sequence 82, Appl  
42 449 81.8 107 1 US-08-899-575-82 Sequence 82, Appl  
43 449 81.8 107 1 US-08-899-575-82 Sequence 82, Appl  
44 449 81.8 107 1 US-08-899-575-82 Sequence 82, Appl  
45 449 81.8 107 1 US-08-899-575-82 Sequence 82, Appl

ALIGNMENTS

RESULT 1  
US-08-812-586-45  
; Sequence 45, Application US/08812586  
; Patent No. 6048704  
; GENERAL INFORMATION:  
; APPLICANT: Martin David Tilson  
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)  
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/812,586  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/53862-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-812-586-45

Query Match 94.4%; Score 518; DB 3; Length 233;  
Best Local Similarity 96.2%; Pred. No. 3e-41;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ELTQSPSSVSASVGDRTVTITCRASQGSQSWLAWYOHQPGKAPKLLIYSASSLSQSGVPSRF 60  
DB 23 ELTQSPSSVSASVGDRTVTITCRASQGSQSWLAWYOHQPGKAPKLLIYSASSLSQSGVPSRF 82

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QY 61 SGGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 83 SGGSGGTDFSLTSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 2
US-09-535-832A-42
; Sequence 42, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilsen, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535.832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-42

Query Match 94.4%; Score 518; DB 4; Length 233;
Best Local Similarity 96.2%; Pred. No. 3e-41; 3; Indels 0; Gaps 0;
Matches 102; Conservative 1; Mismatches 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 23 ELTQSPSSVSASVGDRTVITTCRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 82

QY 61 SGGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 83 SGGSGGTDFSLTSSLOPEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 3
US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934.373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-3

Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLAWYQHQPGRKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQDVSSYLAWYQKPKAPKLLIYVAASSLESSGVPSRF 62

QY 61 SGGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGGSGGTDFLTSSLOPEDFATYCCQYNSLPYTFGGTKVEIKR 108

RESULT 4
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437.642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3
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Query Match      84.9%; Score 466; DB 3; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKPGKAPKLLIYAASSLESQVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGGTDFLTISLQPEDFATYCCQYNSLPYTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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```

RESULT 5
US-08-146-206C-3
; Sequence 3, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-3

```

```

Query Match      84.9%; Score 466; DB 4; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKPGKAPKLLIYAASSLESQVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGGTDFLTISLQPEDFATYCCQYNSLPYTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 6
US-09-705-686-3
; Sequence 3, Application US/09705686
; Patent No. 6639055

```

```

; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3

Query Match      84.9%; Score 466; DB 4; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKPGKAPKLLIYAASSLESQVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGGTDFLTISLQPEDFATYCCQYNSLPYTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
PCT-US93-07832-3
; Sequence 3, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-3

Query Match      84.9%; Score 466; DB 5; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRVITTCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQGVPSRF 60
Db 3 QMTQSPSSLASVGDVRVITTCRASQDVSSYLAHYQKPKAPKLLIYASASSLSQGVPSRF 62

QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 63 SGSGGTDFTLTISLQPEDFATYCCQNSLPYTFGQGTKEIKR 108

RESULT 8
US-09-240-274-40
; Sequence 40, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I09
; US-09-240-274-40

Query Match      84.3%; Score 463; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.8e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRVITTCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQGVPSRF 60
Db 2 ELTQSPSSLASVGDVRVITTCRASQGISWLAHYQKPKAPKLLIYASASSLSQGVPSRF 61

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-3

Query Match      84.9%; Score 466; DB 5; Length 109;
Best Local Similarity 84.9%; Pred. No. 9.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRVITTCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQGVPSRF 60
Db 3 QMTQSPSSLASVGDVRVITTCRASQDVSSYLAHYQKPKAPKLLIYASASSLSQGVPSRF 62

QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 63 SGSGGTDFTLTISLQPEDFATYCCQNSLPYTFGQGTKEIKR 108

RESULT 9
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDVRVITTCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQGVPSRF 60
Db 1 ELTQSPSSLASVGDVRVITTCRASQGISWLAHYQKPKAPKLLIYASASSLSQGVPSRF 60

QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 61 SGSGGTDFTLTISLQPEDFATYCCQNSLPYTFGQGTKEIKR 106

RESULT 10
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2337
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQGISWLNWYQQKPGKAPKLLIYAASLSQSGVPSRF 60
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGQTKVEIKR 106
Db 61 SGSGSGTDFLTITISLQPEDFATYCCQSYSTPYTFQGQTKLEIKR 106

RESULT 11
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2337
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASLSQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQGISWLNWYQQKPGKAPKLLIYAASLSQSGVPSRF 60
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGQTKVEIKR 106
Db 61 SGSGSGTDFLTITISLQPEDFATYCCQSYSTPYTFQGQTKLEIKR 106

RESULT 12
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
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SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-08743-104

Query Match 83.8%; Score 460; DB 5; Length 107;  
 Best Local Similarity 85.8%; Pred. No. 3.5e-36;  
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYASLSQGVPSRF 60  
 DB 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYASLSQGVPSRF 60  
 QY 61 SGSGYGTDFSLTITSLQPEDSATYCCQANSFPYTFGGTKVEIKR 106  
 DB 61 SGSGYGTDFSLTITSLQPEDSATYCCQANSFPYTFGGTKVEIKR 106

RESULT 13

US-08-974-899-3  
 Sequence 3, Application US/08974899  
 Patent No. 6037454

GENERAL INFORMATION:  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Jardieu, Paula M.  
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,899  
 FILING DATE:  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/031971  
 FILING DATE: 11/27/96  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 40,378  
 REFERENCE/DOCKET NUMBER: P1014R1  
 TELEPHONE: 650/225-1994  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

US-08-974-899-3  
 Query Match 83.8%; Score 460; DB 3; Length 108;  
 Best Local Similarity 84.0%; Pred. No. 3.5e-36;  
 Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYASLSQGVPSRF 60  
 DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYASLSQGVPSRF 62  
 QY 61 SGSGYGTDFSLTITSLQPEDSATYCCQANSFPYTFGGTKVEIKR 106  
 DB 63 SGSGYGTDFSLTITSLQPEDSATYCCQANSFPYTFGGTKVEIKR 108

RESULT 14

US-08-259-372A-14  
 Sequence 14, Application US/08259372A  
 Patent No. 5565354

GENERAL INFORMATION:  
 APPLICANT: Ostberg, Lars G.  
 TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL  
 TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/259,372A  
 FILING DATE: 14-JUN-1994  
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/871,426  
 FILING DATE: 21-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/676,036  
 FILING DATE: 27-MAR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/538,796  
 FILING DATE: 15-JUN-1990

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/192,754  
 FILING DATE: 11-MAY-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 06/925,196  
 FILING DATE: 31-OCT-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 06/904,517  
 FILING DATE: 05-SEP-1986  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M.

REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 11823-50-7  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 128 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-259-372A-14  
 Query Match 83.8%; Score 459; DB 1; Length 128;  
 Best Local Similarity 82.1%; Pred. No. 5.2e-36;  
 Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYASLSQGVPSRF 60  
 DB 23 QMTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHQPGRKAPKLLIYASLSQGVPSRF 82  
 QY 61 SGSGYGTDFSLTITSLQPEDSATYCCQANSFPYTFGGTKVEIKR 106  
 DB 83 IGSGSGTDFSLTITSLQPEDSATYCCQANSFPYTFGGTKVEIKR 128



RESULT 15  
US-08-468-671-14  
; Sequence 14, Application US/08468671  
; Patent No. 5648077  
; GENERAL INFORMATION:  
; APPLICANT: Ostberg, Lars G.  
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,671  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/259,372  
; FILING DATE: 14-JUN-1994  
; APPLICATION NUMBER: US 07/871,426  
; FILING DATE: 21-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/676,036  
; FILING DATE: 27-MAR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/538,796  
; FILING DATE: 15-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/904,517  
; FILING DATE: 05-SEP-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-50-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-671-14

Search completed: August 8, 2004, 12:20:25  
Job time : 12.6879 secs

Query Match 83.6%; Score 459; DB 1; Length 128;  
Best Local Similarity 82.1%; Pred. No. 5.2e-36;  
Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISSMLAWYQHQPGRKAPKLLIYSASSLSQSGVPSRF 60  
Db 23 QMTQSPSSVSASVGDRTVITTCRASQGISSMLAWYQHQPGRKAPKLLIHAASSLSQSGVPSRF 82  
Qy 61 SGSGYGTDFSLTITSLQFEDSATYVYCCQANSFPYTFGGTKVETK 106  
Db 83 IGSGSGTDFSLTITSLQFEDSATYVYCCQADSLPFTFGGTKVDFK 128

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